

## **FIGURE 1**

CCAATGCCCGGTGCGGTGGTGCAGGGCTCGGGCTAGTC**ATG**GCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTCAGAGAGCGTTCTGCTAATCTACACTTTATTTC  
TGGATCACTGGCGTTATCCTTCTGCAGTTGGCATTGGGCAAGGTGAGCCTGGAGAATTA  
CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCCTATTGCTACTGGTACCG  
TCATTATTCTTTGGGCACCTTGGTTGTTGCTACCTGCCAGGCTCTGCATGGATGCTA  
AAACTGTATGCAATGTTCTGACTCTCGTTTTGGTCGAACGGTCGCTGCCATCGTAGG  
ATTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAACGCGACTAGACAAGATCCAAACAGTTGCAT  
TGTGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTACTCAGAAAAGGATT  
TCCTAAGAGTTGCTGTAACATTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCCTTGGAGTTGCTGCTTCAACTGATTGGAATCTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGCCTATTCCCT  
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTGGCTGGAGAACTG  
ACAACACTACTGATAGACCAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAAACACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGCTGAT  
TCAATCAAGATGTATGTTGCTATGTTCTAAGTCCACCTCTATCCCATGTTAGATCG  
TTGAAACCCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

## **FIGURE 2**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSVLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

### **FIGURE 3**

CCCACCGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTGCCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCACCGCGCTGCTCTGAGCCCTGGCACGCCAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGAAACAGCCGCTCGAGCCTGGGCCGGGACCGGACTGGG  
GCCGGGGTAGGCCTGGAAAGGGCCGGAGAGAGGGTGGCCTGGTCAGAACCTGAGAAACA  
GCGGAGAGGTTTCCACCGAGGCCCGCCTGAGGGATCTGAAGAGGTTCTAGAAGAGGGT  
GTTCCCTCTTCGGGGTCCTCACAGAAGAGGTTCTGGGGTCGCCCTCTGAGGAGGCT  
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTCTTGGATTCACTGTTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGGAAAAGTACCTAAATGATCGTCTTG  
GTTGGCCGTGTTCTAGCGAGCAGAACGCCCTGGCCAGGGTCTGTTGACTCTCGAAGAG  
CACATAGCCCACCTCCTAGGGACTGGAGGTGCCGCTACTACCATTGGTAATTCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCCTGTCGGCCACCAAGGAGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAATGTGGATGGCTAGTGTGGACACACT  
GGCAGTAATACGGACTCTGTAGATAAGTAAGGTATCTGACTCACGGTCACCTCCAGTGGAAAT  
GAAAAGTGTCTGCCCGAACCATGACTTTAGGACTCCTCAGTCCTTAGGACATACTCG  
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAAATATTAAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTGATGTTTGCTTGCTGTCACTACTTGTCTGGAAATGTCTAAATGTTTC  
TGTAGCAGAAAACACGATAAGCTATGATCTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVVDGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

## **FIGURE 5**

GGCACGAGGCCTGTCACCCGGGGCGTGGAGTGAGGTACCAAGATTCAAGCCATTGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTCGGATTGAGGTCCCGTTCTAACGGACTG  
CAAGATGGAGGAAGGCAGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTCGTCTCAGGCTTCCTGCTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTTCCCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTGGCTCACAGCATGCTGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTACCTGCTGTTCTGAGCCTACGCTGCCACTGTCAAC  
GCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCAAGTACAGTGCTCTCCGCCAGAATTCTTCCGCTACCATGGGCTGTCC  
TCTCTTGCAATCTGGCTGCGTCCTGAGCAATGGGCTCTGCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAATGCTTCTCAGAAATGAAAAAAA  
AAAAAAAAAAA

## **FIGURE 6**

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
MEEGGNLGGGLIKMVHLLVLSGAWGMQMWMVFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLLATVNARWLEPRTTAAMWALQTVKEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTAAGCCCATTCTGCAGTGGATTTCATGAACAGAAGGACACCATCTT  
 CTTGTATTATAACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAA**ATG**CTTTGGGT  
 GCTAGGCCTCCTAATCCTCTGTGGTTCTGTGGACTCGTAAAGGAAAACCTAAAGATTGAAG  
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCC  
 AGAACTTTGATAAAAAGGGATTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
 AGCTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTCTGGATGTGACCGACCCAG  
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGT  
 CTGATCAATAATGCTGGTGTCCCAGCGTGTGGCTCCACTGACTGGCTGACACTAGAGGA  
 CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTTC  
 CTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAAATGTCTCCAGTGTGGAGGTGCCTTGCA  
 ATCGTTGGAGGGGCTATACTCCATCAAATATGCAGTGGAAAGGTTCAATGACAGCTTAAG  
 ACAGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
 ACTTGGCAGATCCAGTAAAGGTAAATTGAAAAAAACTGCCATTGGGAGCAGCTGTCTCCA  
 GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA  
 TAAATCCTATGTGAACATGGACCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
 GTCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAATTCTGGATAACCTCTG  
 TCTCACATGCCAGCAGCTTGCAAGACTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
 TCCCAAGGCAGTG**TGA**CTCAGCTAACCAACAAATGTCTCCTCCAGGCTATGAAATTGCCGAT  
 TTCAAGAACACATCTCCTTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTAGA  
 TCGTGTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGTATCCCAGGGTCCCTG  
 CTCAAGTTCTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT  
 ATTTAGGCTTGCCTGCTGGTGTGATGTAAGGAAATTGAAAGACTTGCCCATTCAAATG  
 ATCTTACCGTGGCCTGCCCATGCTTATGGTCCCCAGCATTACAGTAACCTGTGAATGTT  
 AAGTATCATCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAA  
 AAAAAAAAAAAAAAAA

**FIGURE 8**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAAARTFDKKGFHVIACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVIAPTDW
LTLEDYREPIEVNLFGlisVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV

```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## FIGURE 9

GCAGGGCTGTTGACGGCGCTGCG**ATGG**CTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTCCTGACGCCGCCAGTGGCGGGGCCCTGGGCCGTCGCCACCACT  
 GTAGTCATGTACCCACCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTGGCGGCCGCTCGTGTGGAGGAATGGA  
 AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTCCTGCCTTCTGCTTTCTGT  
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGTTAAAACCAGCAAATCCACCCGCTTACCA  
 CTCCTCAGAAGGCCGACACCCTGAGAACTTACCTGAGATTTCGTACAGAAGACACAA  
 AGACACATCCAGCGGGGACCCCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGGCCCTGTGGATCCCCGCCGGAAAGGAG  
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG  
 CTCCCTCAAGAAGAGCAGAACTGCCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG  
 CACACCAGTGCATCTGAACATCGCCAGAAGGGCGTGATTGACGTCTCCTGCATGCATGGA  
 AAGGATAACCGCAAGTTGCATGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTCAGT  
 GAGTGGTTGGCCTCGGTCTCACACTGATCGACCGCTGGACACCATGTGGATCTTGGTCT  
 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTGAAGGAGC  
 TGGACGTCAACCTGTTGAGAGCACGATCCGCATCCTGGGGGGCTCTGAGTGCCTACAC  
 CTGTCTGGGGACAGCCTCTTGAGGAAAGCTGAGGATTTGGAAATCGGCTAATGCCTGC  
 CTTCAGAACACCCTCAAGATTCTTACTCGGATGTGAACATCGGTAUTGGAGTTGCCACC  
 CGCCACGGTGGACCTCCGACAGCACTGTGGCGAGGTGACCAGCATTAGCTGGAGTCCGG  
 GAGCTCTCCGTCTCACAGGGATAAGAAGTTCAAGGAGGAGTGGCTGGCATGTTCATCA  
 ATCCACGGCCTGTCTGGGAAGAAGGATGGCTGGTGCCATGTTCATCAATACCCACAGT  
 GCCTCTTCAACCACTGGCGTATTACGCTGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAAGCAGGAGACACAGCTGCTGGAAGACTACGT  
 AGCCATCGAGGGTGTCAAGACGCACCTGCTGCCGACTCCGAGCCAGTAAGCTCACCTT  
 TGGGGGAGCTTGCCCACGGCCGCTTCAGTGCCTAGATGGACCACCTGGTGTGCTTCTGCC  
 GGGACGCTGGCTCTGGCGTCTACCACGGCCTGCCAGCCACATGGAGCTGGCCAGGA  
 GCTCATGGAGACTTGTACAGATGAACCGGAGATGGAGACGGGCTGAGTCCCGAGATCG  
 TGCACCTCAACCTTACCCCCAGCCGGCGTCGGACGTGGAGGCTGTTACCTGTACCGCGT  
 CACAGGGGACCGAAATACCAGGACTGGGCTGGGAGATTCTGCAGAGCTCAGCCATT  
 CCTCGGGTGGCTATTCTCCATCAACAATGTCCAGGATCCTCAGAAGGCCGAGCCTAGGG  
 AACATGGAGAGCTTCTCTGGGGAGACGCTCAAGTATCTGTTCTGCTCTCCGATGA  
 CCCAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCCCTGCCT  
 ATCTGGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGCAGAGGCACCT  
 CTGGGTCTGTCATTTCCAAGGGCCACGTAGCAGCGCAACCGCCAAGTGGCCAGGGCT  
 CTGAACCTGGCTCTGGCTCCTCGTCTGCTTAAATCAGGACACCGTGAGGACAAGTGA  
 GGCGTCAGTCTGGTGTGATGCCGGTGGCTGGCCGCTGGAGGCCCTGCCCTGCTCCTC  
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGCC  
 GAGGGGGCTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGAGCAGCCCAGGGTG  
 CAGCCTCTGCCGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGCTGGAGGGCT  
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTGTTACAAGCTGGACTCAGGG  
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 CCAGTGGAAATGGGTCTTCGGTGGAGATAAAAGTTGATTGCTCTAACCGCAA

## FIGURE 10

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><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPHRDFISVTLFGESYDN
SKSWRRRSCWRKWQQLSRLQRNMILFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPDPQRTVISWRGAVIEPEQGTTELPSRRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTLGVFTL GARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFGELAHGRFSAKMDHLCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCTGCGAGGCCCTGCCCATGCGCCGC  
 CGCCTCTCCGACG**ATG**TTCCCTCGCGAGGAAAGCGCGCAGCTGCCCTGGAGGACGGC  
 AGGTCCGGGTTGCTCTCCGGCGCTCCCTCGGAAGTGTCCGTCTCCACCTGTTCGTGGC  
 CTGCCCTCTCGCTGGGCTTCTTCTCCACTCTGGCTGCAGCTCAGCTGCTCTGGGACGTGG  
 CCCGGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCCAGAG  
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGCCCCACCGCCTGGCAGTGCTGGT  
 GCCCTTCCCGAACGCTTCGAGGAGCTCCTGGTCTCGTGCACATGCCGCTTCCTGA  
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTCAGGTTAAC  
 CGGGCAGCGCTCATCAACGTGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
 GCACGACGTTGACCTGCTCCCTCTAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGC  
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCCTCTACCAACTACAAGACCTATGTCGGCGGC  
 ATCCTGCTGCTCTCCAAGCAGCACTACCGCTGTGCAATGGATGTCCAACCGCTTCTGGG  
 CTGGGGCCGCGAGGACGACGAGTTCTACCGCGCATTAAGGGAGCTGGCTCCAGCTTTCC  
 GCCCCTCGGAATACAACACTGGTACAAGACATTGCCACCTGCATGACCCAGCCTGGCGG  
 AAGAGGGACCAGAAGCGCATCGCAGCTAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCGCACTGCCCTGTCTGTGGCGGGGCC  
 CCTGCACTGTCCTAACATCATGTTGACTGTGACAAGACCGCCACACCCTGGTGCACATT  
 AG**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATTGCTCAGGCTCAGGA  
 CAAGGCCTCAGGTCGTGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
 AGCTACGCAATTGCAGCCACCCGGCCAGGCAGGCTGGCTGGCCAGGACACGTGG  
 GTGCCCTGGGACGCTGCCATGCACAGTGTACAGAGAGAGGCTGGGTGTGCCTGTCCG  
 GGACCCCCCCTGCCTCCTGCTCACCTACTCTGACCTCCTCACGTGCCAGGCCTGTGG  
 TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTCACGTGCC  
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 AAAAAA

## FIGURE 12

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGGLPRKCSVFHLFVACLSLGFFSLLWIQLSCSGDVARAVR
GQQQETSGPPRACPPEPPPEHWEEDASWGPRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHIIYVLNQVDHFRFNRAALINVGFLLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAQKQEKFVDRREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

## **FIGURE 13**

CAATTTGCCTATCCACCTCCCCAAGCCCCCTTACCT **ATG**CTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTTAAAGGCTCATGCTGGAGTGGGACTGGTCGGTGCCAGAAAGTCT  
CTTCTGCCACTGACCCCCATCAGGGATTGGGCCTCTTCCCCCTCCTTCTGTGTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT  
GGGGATGGC **TAA**GAAAGCTGGGAGATAGGGAACAGAACAGAGGGTAGTGGGTGGCTAGGGGG  
GCTGCCTATTAAAGTGGTGTATGATTCTTACTAATTATAACAAAGATATTAAGC  
CCTGTTCTTAAGAAATTGTTCCCTCCCTGTGTTCAATGTTGAAAGATTGTTCTGTGT  
AAATATGTCTTATAATAACAGTTAAAGCTGAAAAA

## **FIGURE 14**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862
<subunit 1 of 1, 73 aa, 1 stop
<MW: 7879, pI: 7.21, NX(S/T): 0
MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCQAO
PRGEGEKVGDG
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG  
 GAGCATGTCCCGCCGGGAAGGCCCGTCCCTCCGGCCATAAGGCTCCGGTCGCCGCTGG  
 GCCCGCGCCCGCTCCTGCCGCCGGCTCCGGCGCCATAAGGCTCCGGTCGCCGCTGG  
 CTCGCCCCCGCAGGCCCGCAGC**ATG**GAGCCACCCGGACGCCGGCGGGCCGCGCA  
 GCCGCCGCTGTTGCTGCCGCTCGCTGTAGCGCTGCTCGCCTGCTGGGAGGGCGGGCG  
 GCGGCGGCCGCCGCGCTGCCGCCGGCTGCAAGCACGATGGCGGCCCGAGGGCTGGC  
 AGGGCGGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGCGCAGGTCT  
 GCCCCCAGATACTCTGCCAACCGCACGGTACCCCTGATTCTGAGTAACAATAAGATATCG  
 AGCTGAAGAATGGCTCATTTCTGGGTTAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCTCTGGGACTGTCATCTAAAAAGATTGGATCT  
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTCGAGGACTCACCAATCTGGTC  
 GGCTAAACCTTCGGGAATTGTTCTCATTATCTCAAGGAACCTTGATTATCTTGC  
 TCATTACGGTCTTCCAAGTGCAGACTGAGTATCTTGTGTGACTGTAACATACTGTGGAT  
 GCATCGCTGGTAAAGGAGAACATCACGGTACGGGATACCAGGTGTGTTATCCTAAGT  
 CACTGCAGGCCAACAGTCACAGCGTGAAGCAGGAGCTGTTGACATGCGACCCTCCGCT  
 GAATTGCCGTCTTCTACATGACTCCATCTCATGCCAACGTTGTGTTGAAGGAGACAGCCT  
 TCCCTTCCAGTGCATGGCTCATATATTGATCAGGACATGCAAGTGTGTTGATCAGGATG  
 GGAGAATAGTTGAAACCGATGAATCGAAGGTATTTTGTGAAAAGAACATGATTACAAC  
 TGCTCCTTGATTGCAAGTGCCTAACCATTCTAATATTCAAGGCTGGATCTACTGAAATTG  
 GGGCTGTATGTCCAGACAAACGTGGAATAATACGAGGACTGTTGATATTGTGGTATTAG  
 AGAGTTCTGCACAGTACTGTCCTCCAGAGAGGGTGTAAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTGGCAGGCATTACTGCATATCTGCACTGTACGCGGAACACCCATGGCAGTGG  
 GATATATCCCGAACACCGATGAGAGAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
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 ATGTTAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTGACAGTTACTGGC  
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 TTGAAAATTGGAGATTACCAAGGAGAAAATCAAAGAGCTAGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCCTGTGGCTGGCAGAGGGAAAGC  
 TAAAGCCTGCAGTAGGATTGTGCAGTGTCTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTATTCAACATATTCAACCAATATTGCTCTGGAGCTATGTCATCAAGTCT  
 ACTGGCTTACGGGATGACCTGTACCGTGTCCAGAAAGTGGCAGCCTCTGATCGTACAGG  
 ACTTCGGATTATGGGAGGCAGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTAAAGT  
 GCAATGTTCAAATACATTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATT  
 AAGACTATTACAGT**TA**ATTAGAATGCTCAAATGTTCTGCTCGAAAATAACCTTATT  
 AAAGATTTTTTGAGGAAGATAGGTATTATTGCTTTGCTACTGTTAAAGAAAACCA  
 ACCAGGAAGAACTGCATTACGACTTCAAGGCCCTAGGCATTGGCTTGATCCCTT  
 CTTCACATAAAATACAGAAATTACATTAACTGCACTGGTATAAATGCAAATATACT  
 ATTGTTACATGTGAAAAATTGACTTAAAGTTATTGTTAAAGTATTGTTTTGCTCCT  
 GATTGTTAAGACAATAAGATGTTTACGGGCCCTAAAGTATCATGAGCCTTGGCACTGC  
 GCCTGCCAACGCTAGTGGAGAAGTCAACCCCTGAGACCAGGTGTTAATCAAGCAAGCTGTAT  
 ATCAAAATTGGCAGAAAACACAAATATGTCATATATCTTTTAAAGTATTCA  
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 GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACCTCCAGCACCCCTAATGGAACCACATT  
 TTTTCACTTAGCTTCTGTGGCATGTGTAATTGTTACTCTGCGGTTAAATCTCACAG  
 TACTTTATTCTGTCTGTCCCTCAATAATCACAAACAAATATTCCAGTCATTAAATGGC  
 TGCATAAAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAATA  
 TTGAATGAATGAACGAAAAAA

**FIGURE 16**

MEPPGRRRGRAQPPLLLPLSLLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
 VVCSSLELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
 FWGLSSLKRLDLTNNRIGCLNADI FRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT  
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLCDPPLPEPSFYMTP  
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT  
 ISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITA  
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPNL  
 TNAVATARQLLAYTVEAANFSMDKMDVIFVAEMIEKFGRTKEEKSKELGDMVDIASNIMLA  
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
 VFQKVAASDRTGLSDYGRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
 433-437, 453-457, 592-596**N-myristylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
 384-390, 403-409, 554-560

## FIGURE 17

GC GTGGGG **ATG** TCTAGGAGCTCGAAGGTGGT GCTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTGGAAAAAGAAAACATT CGTCTTTGGGAGAACAGATTA  
TTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAAA  
TCA **TGA** CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTGGTCACTGTCCTTTAAACTGATCA  
AATAAAGGACAGTGGGTCAATAAGTTACTGCTTCAGGGTCCCTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTGGAAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAACGACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAAC  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCAATCC

## **FIGURE 18**

MSRSSKVVLGLSVLLTAATVAGVHV**KQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT**  
EQLEAEREKMLLA**KGSQKS**

**Signal peptide:**

amino acids 1-21

## **FIGURE 19**

CTGTCGTCTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTTACAGCCTGTC  
 CAAGTGTGGCTTAATCCGTCTCCACCACAGATCTTCTCCGTGGATTCTCTGCTAAGACC  
 GCTGCC**ATGCC**AGTGACGGTAACCCGCACCACCATCACAAACCACGACGTATCTCGGG  
 CCTGGGGTCCCCATGATCGTGGGTCCCCCTGGGCCCTGACACAGCCCTGGGTCTCCTTCGC  
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTCTCGCTGGTGGTAGCGTGGCGCCTGGAC  
 GGGGTCCATGGGCAACTGGTCCATGTTCACCTGGTGCTTGCTTCTCCGTGACCGTGTGATCA  
 TCCTCATCGTGGAGCTGTGCAGGCTCCAGGCCGCTTCCCGCTGTCTGGCGCAACTCCCC  
 ATCACCTTCGCCTGCTATGCAGGCCCTCTTCTGCCTCTCGGCCTCCATCATCACCCAC  
 CTATGTCCAGTCCCTGTCCCACGGCCGTTCGCAGGACACGCCATGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGCCGGCCGGCGAG  
 ATCACTGGCTATATGCCACCGTACCCGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
 CATCATCTTCGCGTTCATCAGCGACCCAACCTGTACCGACCCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTACCTAGCGGCCATGCCATCCTGCTGAACCTGGGG  
 GAGTGCACCAACGTGCTACCCATCCCCCTCCCCAGCTTCTGTCGGGCTGGCCTGCTGTC  
 TGTCCCTCTATGCCACCGCCCTGTTCTGCCCCCTCTACCAGTTGATGAGAAGTATG  
 GCGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCACTACGTGTG  
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGCACTCTGCCACCTGGTTTGTCAGGTC**TAA**AGACTCTCCAAGAGGCTCC  
 CGTCCCTCTCCAACCTTTGTTCTTGCCTGAGTTTCTTATGGAGTACTCTTCC  
 TCCGCCTTCCCTGTGTTCTGCTTCCCTGCTCCCCTCCACCTTTCTTCC  
 CAATTCCCTGCACTCTAACCAACAGTTCTGGATGCATCTTCTCCCTTCCCTTGT  
 TTCCCTCTGTGTTGTTGCCACATCCTGTTCAACCCCTGAGCTGTTCTCTT  
 CTTTCTTCTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTGGTCAAGCGATTCTCCTCC  
 CCCAGCCTCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCTT  
 TTCCACTCTCTTTCTCATCTCTTCTGGGTTGCCTGTCGGCTTCTATCTGCTGT  
 TTTGCAAGCACCTCTCCTGTCCTGGAGCCCTGAGACTTCTCTCCCTGCTCCA  
 CCCACCTCAAAGGTGCTGAGCTCACATCCACACCCCTGCAGCCGCTCCATGCCACAGCCCC  
 CCAAGGGGCCATTGCCAAAGCATGCCCTGGGAGGCTGAGCTGGGATTGGGCCCTT  
 GTGTGTGTGTGTGTTGGGGGTGGGGTAGCTGGGATTGGGCCCTT  
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCTTAAATTAAAAACATATATATAT  
 ATTTGGAGGTCAGTAATTCCAATGGCGGGAGGCATTAAGCACCGACCCCTGGTCCCTAGG  
 CCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGGCCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTAAAGGAAGCAGGGCTGGATGCCTTCATCCAACTATTCT  
 CTGTGGTATAAAAAG

## **FIGURE 20**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTSSGLGSPMIVGSPRALTQPLGLRLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALEWCVAVYAIKFILAAIAILLNGETCNVLPIFPFSLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLLAVAILTAINLLAYVAD
LVHSAHLVFKV
```

**Important features:**

**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21

## FIGURE 21

GAACGTGCCACCATGCCAGCTAATTGGTATTTAGTAGAGACGGGTTTACCATGTTGCCAGGCTGGTC  
 TTGAACCTGTGACCTCATGATCGCTCACCTCGGCCCTCCAAAGTGTGGATTACAGGCATGACCAACTGACGC  
 CTGCCAGCCTATGCATTAAAGAAATTATTCTGTATTAGGTGCTGTGCTAAACATTGGCACTACAGTGA  
 AACAGACTGAATTCCCCAAGAGCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAATGCAAAAGAGACCA  
 TTATTACTCACTATGACTAAGGGTACAAATGGGTACGGTGTGAGAGTGTGTTAAGAGACTACAGAGGG  
 AGGACAGACTACCAAGAGGGGCCAGGAAAGCTCTGACGAGGTGGTATTCAGCCAAACTGGAAGAATGA  
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTACACTTTGGCCTGAGAA  
 AATAGCATGGGATTGGAGGAGCTGGGGAACACCACTTCTGCCGACCTGGGAGGGCATTGAGGGCTTGAGA  
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTGAGGTGGAAATCATTAGGTCTTATC  
 AACAGATATGGCAAGCAAAGCCAGGGAGAAATTGATGTTAATGCTGAGGTTGGAGCCAGGCTAGATGGACAG  
 TGGTGGGTGATGCAAAGGAAAGAGGTCAAGGAAGCAGGGCAGACGTGGGAGAAGGTGTGGGGTTGGTTCCA  
 TCTTGGCAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGCAGAGGGAAAGGGAACTTAA  
 AGAAGTCTGGATGCCACACTCTTCTCCTCTCCCTCTCAGAGGTCTCACTCGTGGTCTTCT  
 TTCTGCCCTGCCCTCATCTCTGGGTGCTGGAAAGTGGAGGATTAGCTGAAGTTGCTTCTCGGGCCTG  
 TCTGAATCTCATTGCTTCTGGGAGGACATAATTACCTGTCTAGCTTCTATCATCTTACATTCCCTGTAG  
 CCACGGGACATATGTGGTGTCTCTAGCTCCTGTCTCCTCATGCCTTGCTGGGTATGGCATGTTAG  
 GGGGAAGGTATTGCTGTAGACGGGCACTGACTTTCTAATGGTGTACCCAAGGTGAATGTTGGAGACACAGTC  
 GCGATGCTGCCAAGTCCCGGAGGCCAACTATCCAGGAGATCGCTGCGCTGCCAGGTCCCTGCATGGT  
 ATGCAGCCCCCTCC~~ATG~~TCTGGCAACTTGTCTTCTCTCCCTGTTGCACATCCCTTGGAACTGTTCT  
 GTGAGTACATGTTGGGCTCTCCCTTCTTCCCTGTCTAGGTGAATCTCAGCCCCCTCTCCACCCAAAGGTT  
 ACATGGATCCTAACTACTGCCCCCTCCACCTCCCTGCACCTGTGCTCCCTGGCTGGTCTTACCAAGGCTT  
 TCCACCCCTCCCTATCTCAGGTATTCCCAGGTGGTGAAGGACACGTGACCAAGCCTACGCCATGCCAGG  
 GCCGAGTGGCTCACCTATTGAGTGGAAAGGGCTGGAGCAAGCCGAGTGAACCTGCTGCCCTGGAAATCAGCCT  
 TTTCTCTTATCAGACCTCAGCGAGGGCAACAAAGAGGCTGGCTTGCAGCAGGAGTGGCTGAGCAGTTGCCA  
 TCGCGGAAGCCAAGCTCCGAGCATGGTCTCGGTGGATGGCAGGACTCCACTGACTCCTATGATGAGGACT  
 TTGCTGGGGAAATGGACACAGACATGGCTGGCAGCTGCCCTGGGGCGCACCTCAGGACCTGTTCACCGGCC  
 ACCGGTTCTCCCGCCTGTGCCAGGGCTCCGGAGGCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA  
 CCCTGTGCTCTAGTCTGTGCAAGCTGGAGGATGGTTGTTGGCTCCCGGCCGGCTGGCTCCAGCTGCTGG  
 GCGATGAGCTGCTCTGCCAAACTGCCCTGGGGAAAGTGCCTTCCGAGCCTGGGGCCACTGGAGGGCCC  
 AGGACTCACTCTACAACCTGCCCTCACAGAGTCCTGCCTTCCCCCGCGAGGAGGAGGCCAGCCCCCTGCAAGG  
 ACTGCCAGCCACTCTGCCACCAACTACGGGAGCTGGGAACGGCAGCGCAAGCCTGTACCTGGCTCTTCTG  
 GGGTGGTGTCTTAGATGAGGATGAGGAGCAGAGGAACAGTGAACCATCATGCCCTGGCAGTGGCATGCA  
 TCCCCGGCTGCTGCCAGGGCAGAGCCTGTGCCAACAGTGTGGCTCAAGGCTCCAGCAGAGCTCCACAGCC  
 TAGAGGGCTCTGGGAGCGCTCGCTTCTCGTTGTGTTTGATGAAAGTGTGAGAGGGAGGCCAGGGCTG  
 GGCTGGGGCGCATGTCTGCCCTACTCCGGGCTTGCCGGGGCTCTGGGCTATGGCTACA  
 GCTGTGGCAGACAGTGTGATGTTCATGTTCTAAATGCCACACACATTCTCTCGGATAATGTGAACCACTA  
 AGGGGTTGTGACTGGCTGTGAGGGTGGGGTGGGAGGGGCCAGCAACCCCCCACCCTCCCCATGCCCTC  
 TCTCTCTGCTTCTTCTCACTCCAGTCCACTGTCAGTGCTGATAGAATCACCCCCACCTGGAGGGCTGG  
 CTCCCTGCCCTCCCGAGCCTATGGGTGAGCCGCTCCCTCAAGGGCCCTGCCAGCTGGCTCGTGTGCTTC  
 ATTACACCTCTCCATCGTCTCTAAATCTCCTTCTTCTAAAGACAGAAGGTGTTGGCTGTTTCTCAGTC  
 GGATCTCTCTCTGGAGGCTTGGAAATGATGAAAGCATGACAGTGTGACCTCCACCCCTTCTGGCCCTTAATGG  
 GGCCTGGGCCCTTCCAACCCCTCTAGGATGTGCGGGCAGTGTGCTGGCGCTCACAGCCAGCCGGCTGCC  
 ATTACAGCAGAGCTCTGAGCGGGAGGTGGAAAGAAAGGATGGCTGGTTGCCACAGAGCTGGACTTCTGTT  
 CTTCTAGAGAGGGCACAAGAGGGCACAGGGGTGGCGGGAGTTGTCAGCTGATGCCCTGTGAGAGGGAGGAAT  
 TGTGCCAGTGAAGTGAACAGTCAGGGAGTGTCTTCTGGGGAGGAAAGAAGGTAGAGCCCTTCTGCTGAAT  
 GAAAGGCCAAGGCTACAGTACAGGGCCCCGCCAGCCAGGGTGTAAATGCCACAGTAGTGGAGGCCTGGCAG  
 ATCCCTGCATTCCAAGGTCACTGGACTGTACGTTTATGGTGTGGAAAGGGTGGCTTAAAGAATTAAAGGC  
 CTTGTAGGCTTGGCAGGTAAGAGGGCCAAGGTAAAGAACAGAGGCCAACGGGACAAGCATTCTATATAAGT  
 GGCTCATTAGGTGTTATTGTTCTATTAAAGAATTGTTTATTAAATTATAAAAACTTTGTAATCTC  
 TAAAAA

## **FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSFPSHPKVHMDPNYCHPSTSLHLCS  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESAFSSY  
SDLSEGEQEEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

## FIGURE 23

GGTTCCCTGGCGCTCTGTTACACAAGCAAGATAAGCCAGCCCCACCTAATTTGTTCCCT  
 GGCACCCTCCTGCTCAGTGCAGACATTGTCACACTAACCCATCTGTTTCTTAATGCACGA  
 CAGATTCCCTTCAGACAGGACAACGTGATATTCAAGTCTGATTGAAATACCTCCTAAG  
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTCAGTTCTCATCTGAAAATGGGCATAA  
 TACAATCTATTCTGCCACATCAAGGGATTGTTATTCTTAAAAAAACCAATACCAAAG  
 AACGCTACAA**ATG**TTGGCCTTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT  
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTTT  
 TTAAAACAATGGAAAATAAACCTATTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA  
 GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTGAATCTACCCAAACAA  
 CAGCCACGGAATAACAGATTCTCCAGTAACACTCATCAGCAGAGCATTCTTGGCAGTCTAA  
 AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTCTAAAGTGCCT  
 TGGAAATGCACCTATAGCAGATGAAGATCTTGCCATCTCAGCACATCCCAATGCTACACC  
 TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTGGTCAATGACACCGTGAAAACCTCTGATA  
 ACAGTTCCATTACAGTTAGCATCCTCTTCAGAACCAACTCTCCATCTGTGACCCCTTG  
 ATAGTGGAACCAAGTGGATGGCTTACCAACAGTGAAGTAGCTTCACTGGTTACCCCTTA  
 TCAAGAAAAACAACTCTACAGCCTACCTAAAATTCAACAAATAATTCAAACACTCTTCCAA  
 ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGCCATTTAGGT  
 GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGCTACTTGTGTGGAAAAGGAAAAC  
 GGATTCAATTCCCCTCGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
 ATGCACCGGAACCTTATGATGTGAGTTGGATTCTAGCTACTACAATCCAACCTTGAAT  
 GATTGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC  
 TCCACTTCGTACTCTGTA**TAG**AACTAACAGAAAAAGGCCTAACAGCAAGTGTCTA  
 CATCCTAGCCTTGTACAAATTCTTCAAAAGGTACACAAAATTACTGTCACGTGGAT  
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
 CCAAAGGTTTCTTCTTACAATTGGCCATCCTGAGGCATTACTAAGTAGCCTTAATT  
 TGTATTCTAGTATTCTAGTAGAAAATTTGTGGAATCAGATAAAACTAAAGATT  
 TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAATTATTCCACCAAAATTCTAAA  
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCATATTCAAGATTGCAT  
 TTTCTTAAATGAAAATTGAAAGGGTGCTTTAAAGAAAATTGACTAAAGCTAAAAGAG  
 GACATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAATGACAGACCTGTATT  
 TAGTACGTTATAATTCTAGATCAGCACACACATGATCAGCCCCTGAGTTATGAAGCTGA  
 CAATGACTGCATTCAACGGGGCATGGCAGGAAAGCTGACCCCTACCCAGGAAAGTAATAGCT  
 TCTTAAAGTCTCAAAGGTTGGAAATTAACTTGTCTTAATATATCTTAGGCTTCAA  
 TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

## **FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKT MENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSN SSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLT LVGYLLCGKRKTDSF SHRR LYDDRNEPVL RDNAPEPYDV SFGN SYYNPTLNSA
MPESEENARDGIPMDDIPPLRTSV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

## **FIGURE 25**

AACAGGATCTCCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCGAAGATTCACTATGGTGAAAATCGCCTCAATACCCCTACCGCCGTGCAAAAGGAGG  
 AGGCAGCGCAAGACGTGGAGGCCCTCCTGAGCCGACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCTTCATTCATCTTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT  
 TCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCCTGCA  
 AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTGTGATAGTGACCCCTGCA  
 CAATTATTGACTTGAAAAGGAATGACTGCTTACCTGGACTTGTGCTGGGAAGTGC  
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTGCTG  
 TGGAGGAAATTGATGTTAGTAACCTTGGCATCTTATTACCAACTTGCAATAACAGA  
 AAGTCCTTCCGCCTCGTCGCAGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAGT  
AAGAGGCAACAGATAGAGTGTCTGGTAATAAGAAGTCAGAGATTACAATATGACTTAA  
 CATTAAAGGTTATGGGATACTCAAGATATTACTCATGCATTACTCTATTGCTTATGCTT  
 AAAAAAAGGAAAAAAACTACTAACCAACTGCAAGCTCTGTCAAATTAGTTAAT  
 TGGCATTGCTTGTGAAACTGAAATTACATGAGTTTCATTTCCTTGCAATTAG  
 GTTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAATTCCATTCC  
 GTTGTGTTGTTGTTGTTGTTCTTCTTCAAGTAAGCTCTTATTGATCTTATG  
 GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACTTTGTGAAATTATA  
 TCAGATCTAACATTGTTGGTTCTTGTGTTTCATTGTACAACCTTCTGAAATTAGA  
 AATTACATCTTGCAGTCTGTTAGGTGCTCTGTAATTAAACCTGACTTATGTGAAACAAATT  
 TTCATGAGACAGTCATTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTG  
 AATGCACAAAATTGTTAGGTGCTGAATGCTGTAAGGAGTTAGGTTGATGAATTCTACAA  
 CCCTATAATAAAATTACTCTACAAAAA

## **FIGURE 26**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSIRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIIHDFEKGMTAYLDLLLGNCLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFRLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

## FIGURE 27

GGAGGGAGGGAGGGCGGGCAGGCAGCCAGCCCAGAGCAGCCCCGGGACCAAGCACGGACTCTCT  
 CTTCCAGCCCAGGTGCCCTTCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC  
 AAGGAACCTGGCCTGGGGCACCATGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTCTG  
 TTGCTGCTGCTGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT  
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
 CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCTGGGG  
 GGCCCATCACCCCCCACCAACTCCTGGATGGATAGTGGACTTCTCCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGCTCCCTGGCCTTCTGCTGATGTTATCGTCTGTGCCCGGTCA  
 TCACCCGGCAGAACAGCAGAACGGCCTGGCCTATTACCCATCGTCTTCCCCAAGAACAGTAC  
 GTGGACCAGAGTGACCGGGCCGGGGCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCCCTCCGGCAGCTCCAGGCCGACATCTGGCG  
 CCACCCAGAACCTCAAGTCCCCCACCAAGGCTGCACTGGCGGTGGGACGGAGCCAGGATG  
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAAGGGCAGCCAGGAGGGGACCAGGAAGTCCA  
 GGGACATGGGTCCCAGTGGAGACACCAGAGGCCAGGAGGAGCCGTGTCAGGGTCCTTG  
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTTGTAGCCCAG  
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCTGTGCTGCAGCAGTGTCCACCCAG  
 TGTCTAACAGTCCTCCGGCTGCCAGCCCTGACTGTCGGGCCCAAGTGGTCACCTCCCC  
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTGGCCTCCGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
 GGAATCTTACCAAGTGCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
 ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGCTGGATTACAGGCAGGCCACCGTGCCCGGCCAAACTACTTTTAAACACA  
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGAAAATACTGCTCTTAATTTCCTGAAGG  
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGCATTAAATCCTC  
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG  
 GATCAGGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCAAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTGAGGGGACCTCCACCTGGGAAGTCCGAGGGCTGGGAAGGGTTCTGACG  
 CCCAGCCTGGAGCAGGGGGCCCTGCCACCCCTGTTGCTCACACATTGCTGGCAGCCTG  
 TGTCCACAATATTGTCAGTCCTCGACAGGGAGCCTGGCTCCGTGCTGTTAGGGAGGCT  
 CTGGCAGGAGGTCTCTCCCCCATCCCTCATGGGGCTCCCCAACCTCTGCACAGCTCT  
 CCAGGTGCTGAGATATAATGCACCAAGCACAATAAACCTTATTCCGGCCTGAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

## **FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSILLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVTQGHGPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLQAQEAQGPVGPPESPCACSSVHPSV
```

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

## **FIGURE 29**

**FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQGQNPGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSGSSGSSGSSGSSGSSGSSGSGSNGSGSRGDSGSESSW
GSSTGSSSGNHGGSGGGNGHKGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGMFNFTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## FIGURE 31

GACCGGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGCGGTGCTCACCG  
 TGCCCTGGCTGGAGTTCTCTCCTTGCTGACCATGTTGTCCTTGCTGGAATATTACCGGGACATCTTCA  
 CTCTCCTGCTGCGCCTGCACCGAGCTTGGTGTGCGCAGGAGAGTGAGGGAAAG**ATGT**TGTTCTGAACAAAGC  
 TGCTGCTACTTGCTGCTGGCTGGCTTCCAGATTCCCACAGTCCCTGAGGACTTGTCTTCTGGAAGAGG  
 GTCCCTCATATGCCTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTGGACATACTGGCTGCGCTGTGGTGGACCAGC  
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGAAACTGCTCGCTCGTGGGTGTCAGGCAGTAGTG  
 GACGGAGTGGGGCTTCATGAGGAAATCACCCCCACCACTACCACAGCCTGGAGGCCAGCCTTCCCAGACCA  
 GCCAGGGCTGCAGGCACAGCTGCCAGGCCCTTCCACAACCAGCCGCTCCTGCGCCGGACCCTAGAGT  
 TCGTGGCAGAAAGAATTGGATCAAACATGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCAGCAG  
 CAGAGTCACCTCTCCAAGAGCAGCTGGTACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTGGAGATCT  
 TGTGTTCCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAGGAAAGGCCCTG  
 GGGCTGTGCGGGCGTCTCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTCAGAGAACATTGCTGTGGGC  
 TTGCAACAGAGAAAGCCTGTGCTTGCTGTCAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG  
 TGAGTCGACACTTCGAGCCAGGGCTCTGAAACCTGCTGCCCGGGGAGCGGAGGGGCTGCTCCCGGCC**TGAC**  
 GTGCTCTCCTTGGCGTGGGCCACGGGACCTGACGAGGAGTCTCCCAGAGCATCTGAAACAGCTCCTAGGC  
 CAGCTGGGCCAGCAGCTGCCAGTCCCTGTGCCCACCTGCTGAGCAGCATCTGCAAAGTGTCTGTG  
 GAGTTAGCTCCCTCCTCGTTGCAAGATCAAATTCTATCTAGGGCCCCGGCACAGTACAGGCTGGAGAGAGGG  
 CAGGCTCGAAGGCTCTGCACATGCTGCTTCTGTGAGAAGACTTCAGGGCCGGTCCGCTGAGCTG  
 CTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGACTTGCTGCTATTCTGCTA  
 CGGGAGCTGGTGGAGAAGGGTCTGATGGACGGATAGAGGCTGCCTGGCAGCCTCACCAGGCCAG  
 TGGCCAGGGAGCTTGTGAGAAGAAATTAGCAACACTGTCTAATCTGTTCTAGCCGAGCCCACCTGCCAGAACCC  
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGACTGTGCTGCCAGAGCTAGGGCTGAGAAGTGGCC  
 CTGCTTGGGCATTGACCCAGAACCTGGACCCCCGCCCTCACGAGGAGGCCAAGTGCCTGAGAACCCCTCAC  
 TGGTGGGTGAGCTGGCTCAGACTCAGACTTCTGCTAAGGGTGTACTGCCTGGCATCCCACACGC  
 ATCCAGAGGAAGGAGAGTTGGCTGATTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCTGGAGTAGAA  
 GAGGTGGTGTGTTGTTATCTCTGGACTAAATGAAATGAGGTGTGTTGCTGCAACACAGAACATTCAAGCCT  
 CATTGCTATCCCAGCATCTCTAAACTTGTAGTCTTGGAAATTGACAGAGGCCAATGACTCCTGCTTAAC  
 TTATGAAAGAAAGTTAAACATGAATCTGGGAGTCTACATTCTTCTATCACAGGAGCTGGACTGCCATCTCCTT  
 ATAAATGCCTAACACAGGCCGGTCTGGTGGCTCATGCCCTGTAATCCAGCACTTGAGAGGCCCTGAGGTGGCG  
 GACTGCCTGAGGTCAAGAACAGCCTGGCCAACATGGCAAAACCCATCTCTACTAAAAAATAAAAAAA  
 TTATTAGCTGGCATGGTGTGTCCTGTAATCCCAGCTACTCAGGAGGATGAGGAGCAGGAGACCTGCTTGAAC  
 CTGGAGGTGGAGGTTGCACTGAGCCAGGTGCACCACACTGCACTCCAGTCTGGTAACAGAGCAGACTTCTAG  
 AAAAGCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTTCAGGCCCTG  
 TGCAGGTAGTAACCTCTGAGACCTCCCTGACCAGGGACCAAGCACAGGGCATTTAGAGCTTTTAA  
 CTGGTTTCTTAAAGGGCTTTTATTAAATCTCCCCACAGATGGCTCTGCAATCTGCCACAGCTC  
 TTTTTTTTTTTAAAGGGCTTTTATTAAATCTCCCCACAGATGGCTCTGCAATCTGCCACAGCTC  
 TGGGGCTGTCTGAGGAAAGGCCCTGTTTCCCTGAGGCGGGCTGGCTTGCCATGGTCCGGAGCTG  
 GCCGTGCTGGGCCCTGGCGTGTCTAGCTGCTCTTGCCTGGCACAGAGCTGCGGGCTCTGGGGGCC  
 AGCTAACAGAGCAGCTCTGGTGCAGGGCTGGAGGGCTGTCTCTAACCGACACCCCTGAGGTGCTCTGAGATGCTG  
 GGTCCACCCCTGAGTGGCACGGGAGCAGCTGTGGCCGGTCTCTCYTAGGCCAGTCCTGGGAAACTAACGCTC  
 GGGCCCTTCTTGCACAAAGACCGAGGATGGGGTGGGTGTGGGGGACTCATGGGAATGGCCTGAGGAGCTACGTGT  
 GAAGAGGGCGCCGGTTGTTGGCTGCAGCGGCCCTGGAGCGCCTCTCCCTGAGCCTCAGTTCCCTTCCGTCTA  
 ATGAAGAACATGCCGTCTGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTGGACGAGCGTC  
 GTTATTTCAACACTGTCCTGCGACGTTGGCTGGCACGTCTAACGATGGCCTGGACGAGCGTC  
 GTCGCGGTGGAGTGGCAGCCAGAGGCGGGGCCAGACGTGCGCTGGGGTGAAGGGAGGCGCCCCGGAGGG  
 CCTCACAGGAAGTGGGCTCCCGCACCACCGAGGCCAGGGCTCCCGCCGCCGCCACCACCGTCCAGG  
 GGCGGTAGACAAAGTGGAGTGCCTGCGCTGGCTGCGCAGCAGGTAGCCCTTGATGCAGTGCAGGAGCGCG  
 TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACCAGCACGAACAGCCGGTGCCT

## **FIGURE 32**

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTSLGAQPSQTSQGLQAQAFFHQNQPP  
SLRRTVEFVAERIGSNCVKHIKATLADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL  
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282

## FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGTCTACTGAAGGCTGTCTGATCAGGAAACTG  
 AAGACTCTCTGCTTTGCCACAGCAGTCCTGCAGCTCCTGAGGTGTGAACCCACATCCC  
 TGCCCCCAGGGCCACCTGCAGGACGCCACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**  
 AGTAGCAACAAAGAGCAGCGGTAGCAGTGTGATCCTCTTGCCCTCATCACCACCT  
 CATCCTCTACAGCTCCAACAGTCCAATGAGGTCTTCATTACGGCTCCCTGCGGGCGTA  
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
 ACAAGACACTGCCCTCGGTGCCACAGTGTGATTGTCAAGCAGCTCCAGCCACCTGCT  
 GGGCACCAAGCTGGGCCCTGAGATCGAGCAGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACCTACCGCGTGTGGCCCATTCC  
 AGTGTGTTCCCGTGTGAGGAGGCCAGGAGTTGTCAACCGGACCCCTGAAACCGTGT  
 CATCTTCTGGGGGCCCGAGCAAGATGCAGAAGCCCAGGGCAGCCTCGTGCATGATCC  
 AGCGAGCGGGCCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCGCATCGG  
 CAATTGACGACCTTCCGGGTGAGACGGCAAGGACAGGGAGAAGTCTCATTGTGGTT  
 GAGCACAGGCTGGTTACCATGGTATCGCGGTGGAGTTGTGACCACGTGCATGCTATG  
 GCATGGTCCCCCCTACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCAACTAC  
 TACGAGCCAAGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG  
 CAACCACCACCGCTCATCACCAGAAAAGGGCTTCTCATCGTGGGCCAGCTGTATGGCA  
 TCACCTTCTCCCACCCCTCGGACC**TAG**GCCACCCAGCCTGTGGACCTCAGGAGGGTCAG  
 AGGAGAACGCCTCGCCCAGCGCTAGGCCAGGGACCATCTCTGGCAATCAAGGCTTG  
 CTGGAGTGTCTCCCAGCCAATCAGGGCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
 TGGGAATCTGTTGGGAATCAGGGATTGGAGTCTATGTGGTTAATCAGGGGTGTCTTC  
 TTGTCAGTCAGGTCTGCGCACAGTCATCAGGGTAGAGGGGGTATTCAGTCAATCTG  
 AGGCTAAGGACATGTCTTCCATGAGGCCTGGTTCAGAGCCCAGGAATGGACCCCCCA  
 ATCACTCCCCACTCTGCTGGATAATGGGGCTGTCCCAAGGAGCTGGAACTTGGTGT  
 CCCCCCTCAATTCCAGCACCAGAAAAGAGAGATTGTGTTGGGGTAGAAGCTGTCTGGAGGCC  
 GGCCAGAGAATTGTTGGGGTTGTGGAGGTTGTGGGGCGTGGGGAGGTCCAGAGGTGGGA  
 GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTTGGACAAACCTTCCACCTCCCTACAA  
 CACCTTCTGCCACACCAGTTCCAGTGCAGGACTCTGGACCCCTCCAGCCACTATCCCTGCTGG  
 CAGCTCTTGGGGGTCTGGGTGACCTCCCCACCTCCTGGAAAACCTTGTAGGGTATTTGC  
 GCAAACCTCCTCAGGGTTGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTTCT  
 TAGCCCCCTAGCCAGCTGCCATTAGCTGGCTCTAAAGGGCCAGGCCTCCTTTCTGCCCT  
 CTAGCAGGGAGGTTTCCAATGTTGGAGGCGCCTTGGGGCTGCCCTTGTCTGGAGTCA  
 CTGGGGCTCCGAGGGTCTCCCTGACCCCTCTGCGTCTGGATGGCTGTGGAGCTGT  
 ATCACCTGGTTCTGCTCCCTGGCTCTGTATCAGGCACCTTATTAAAGCTGGGCCTCAGTGG  
 GGTGTGTTGTCTCTGCTCTGGAGCCTGGAAGGAAAGGGCTCAGGAGGAGGCTGTGA  
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGTGATGGGTGG  
 GGGCGGTGACTGCCCAAGACTGGTTTGTAAATGATTGTACAGGAATAAACACACCTACGC  
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 34**

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCVIVSSSSHLLGKLGPEIERAECTIRMNDAPTGYSADVGNKTTYRVVAH  
SSVFRVLRRPQEfvNRTPETVFIFWGPPSKMQPKQGSLVRVIQRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIABELCDHVHVVGMVPPNYCSQRPRLQRMPYH  
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

## FIGURE 35

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACCTCAGCGGACCGGGAGCGACGCAGCTT  
 GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGCGAGGCTGAAGCCGAGTGGCCGAGGTGTCGAGGGCTGG  
 GGCAAAGGTGAAAGAGTTCAAGAACAGCTCTGGAACCCATGACCCATGAAGTCTTGTGACATTATACCGT  
 CTGAGGGTAGCAGCTGAAACTAGAAGAAGTGGAGTGGCTGCCAGGGACGGCAGTATCTCTTGTCGACATTATACCGT  
 GGCTATGGGACGTTGGCTTCAGACCTTGTGATACACC**ATG**CTGCGTGGGACGATGACGGCGTGGAGAGGAATG  
 AGGCCTGAGGTACACTGGCTTGCCTCCTAGCCACAGCAGGCTGCTTGACTTGAACGAGGTCCCTCAG  
 GTCACCGTCCACCGCTGCGTCCACGGACTGTGATCTGGGCTGCGTGGTGGAAACCTCCA  
 AGGATGAATGTAACCTGGCGCCTGAATGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCCTCATCACC  
 CACGGGACCCCTCGTCATCACTGCCCTTAACAAACACACTGGGACGGTACCGAGTGTGTCGAGGAGGCG  
 GGGGCTGTGGCAGCGTCCCAGCCACTGTGACACTAGCCAATCTCCAGGACTCAAGTAGTGTGACGACGTG  
 ATTGAAGTGGATGAGGGAAACACAGCAGTCAATTGCGTGCACCTGCGTGGAGAGCCACCCAAAGCCCAGGTCCGG  
 TACAGCGTCAAACAAGAGTGGCTGGAGGCTCCAGAGGTAACACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGCCAGGAGGACGAGGCTACAGTGTGACGCCCTACAACCCAGTGACCCAGGAAGTGA  
 ACCCTCCAGGCTCCAGCAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCGATCATCTACCCCCCAGAGGCC  
 CAAACCATCATCGTACCCAGGCCAGACTGTGACACTAGCCAATCTCCAGGACTCAAGTAGTGTGACGACGTG  
 ACCTGGGCAAGGATGGTCCAGTGTGACCGCTACAAACAAGACGCCCTCTCGTGGAGCAACCTCCATCGAC  
 ACCACCAGCAGGAGGACTCAGGCACCTACCGCTGTCATGGCGCAACATGGGTTGGGAGGCCGGGGAGCGGTG  
 ATCCTCTACAATGTCAGGTGTTGAACCCCCCTGAGGTACCATGGAGCTATCCAGCTGGTCATCCCCCTGGGGC  
 CAGAGTGCAAGCTTACCTGTGAGGTGCGTGGGAAACCCCCCGCCCTCCGTGTCGAGGAAATCCACGGGTC  
 CTCATCTCCAGCCAGCGCTCCGGCTCTCCCGAGGGCCCTGCGCGTGCAGCATGGGCTGAGGACGAAGGC  
 GTTACCGTGCATGCCAGGAGGTGGAGCGCCATGCGTAGTCCAGTGCAGGACCTCCAGGCCAAG  
 ATAACCCCCAAGGCTATGCCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATCACCTCCAAACTCGGCAAC  
 CCTGAGCAGATGCTGAGGGGGCAACCGCGCTCCCCACAGCCCCAACGCTAGTGGGCTGCTTCCCCGAAGTGT  
 CCAGGAGAGAAGGGGCAAGGGGGCTCCCGCCAGGCTCCCATCATCTCAGCTGCCCGCACCTCCAAGACAGAC  
 TCATATGAACTGGTGTGGGGCCTCGGATGAGGGCAGTGGCGGGCGCAATCTCTACTATGTGGTGAAACAC  
 CGCAAGCAGGTACAAATTCTCTGACGATTGACCATCTCTGGCATTCCAGCAACACCAGCACCGCCTGACCC  
 ACCAGACTTGACCCCCGGAGCTGTATGAAGTGGAGATGGCAGCTACAAACTGTGCGGGAGAGGGCCAGACAGCC  
 ATGGTCACCTTCCGAACTGGACGGCGCCCAAACCCAGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC  
 GACCTGGAGCCAGTCCCAGAGCAGCAGCCAGACACGCCGCGCTCTCCCCCGAGAAGCTCCCGACAGG  
 CCCACCATCTCACGGCCCTCGAGACCTCAGTGTACGTGACCTGGATCTCCGGTGGGAATGGTGGTTCCAATC  
 CAGTCCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGAGACTGGATTCTGGCCACAGGCCATCCCCCA  
 TCGCGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCTACAAGTTGAGTCCGGCTCTGAACATG  
 CTGGGGGAGAGCGAGGCCAGCGCCCTCTCGGGCCCTACGTGGTGTGGGCTACAGCGGTGCGTGTACGAGAGG  
 CCCGTGGCAGGTCTTATATCACCTTACGGATGCGTCAATGAGACACCACATGCTCAAGTGGATGTACATC  
 CCAGCAAGTAACAACACCCCCATCCATGGCTTTATATCTATTATGACCCACAGACAGTACAATGATAGT  
 GACTACAAGAAGGATATGGTGAAGGGAGAACACTGGCACTTCAATCAGGCCACCTGCGAGGCCAGAGACCTCTAC  
 GACATTAAGATGCACTGCTTCAATGAAGGGAGGGAGAGCGAGTGTAGCAACAGTGTGATCTGTGAGACCAAAGCT  
 CGGAAGTCTCTGGCCAGCCTGGTCACTGCCACCCCAACTCTGGCCCTACACAGGCCCTTCTGAAACC  
 ATAGAGCGGCCGGTGGCACTGGGGCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGGGGCTGTC  
 CTGGGCTCCATCGTTCTCATCATCGTCACTTCACTCCCTCTGCTTGTGGAGGGCTGGTCAAGCAAAACAT  
 ACAACAGACTGGTTTCTCGAAGTGGCTTCCACCCCTCTGCCGTATACTATGGTGCATTGGGAGGACTC  
 CCAGGCCACAGGCCAGTGGACGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG  
 AATAGGGGCTGCCCTCGGCTGAGTGGGCTACCGGGCATGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCA  
 CAGCAGAGTGAACCCAGCAGCCTGCTGAGGCAGACCCATCTGGCAATGGATATGACCCCCAAAGTCACCA  
 ACGAGGGTCCCAAGTCTAGCCGGACGAGGGCTTTCTTATACACACTGCCGACACTCCACTCACAGCTG  
 CTGCACTGCCGACACTGCTGCCAACGCCAGGAGCAGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC  
 CCCGACAGTCTGCTGGAGACAGTCTGACTCTGCCAAGTGTGAGTGGAGGGACTGGTGTCCCCAGCACCC  
 CCAGTGTGGAGGGTGGACAGTCTGACTCTGCCAAGTGTGAGTGGAGGGACTGGTGTGGGCTTGTG  
 GCCTACGTAGGACAGGAAACCTGGAAATGCACTCTGCCAGGCTGGGCGGGGACTGGTGTGGTGTG  
 CTCACAATT**TAG**GCAGAAGCTGATATCCAGAAAGACTATATTGTTTTTTTAAAGAAGAAAAAA  
 AGAGACAGAGAAAATTGGTATTATTCTATTATAGCATATTATATATTATGCACTTGTAAATAATGTA  
 TATGTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTGGAGAGGGAAAATAAGAAGCTGCCA  
 CCTAACAGGGAGTCACCCAGGAAAGCACCGCACAGGCTGGCGGGACAGACTCCTAACCTGGGCTCTGCA  
 GCAGGCAGGTGCAAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTCATCAGGCA  
 TGAGGGAAACAGCAAGGGGACGGTATCACAGCCCTGGAGACACCCACACAGATGGCTGGATCCGGTGT  
 ACATTTCTAAGATGCCCATGAGAACAGACCAAGATGTGACAGCACTATGAGCATTAAAAACCTTCAGAAT  
 CAATAATCCGTGGCAACATATCTGTAAAAACAAACACTGTAACCTCTAAATAATGTTAGTCTCCCTGTA  
 AAAA

## FIGURE 36

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGCVVEPP  
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLVRRSTAEEAARIIYPPEAQTIIVTKGQSL  
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLSNNLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCERGNPPPSVLWLRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCMANEVGSAAHVQLRTSRPSITPRLWQDAELATGTPVSPSK  
 LGNPEQMLRGQPALPRPPTSGPASPCKPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVVKHRKQVTNSSDDWTISGIPANQHRLTLTRDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTRGRRPKPEIMASKEQQIQRDDPGASPQSSQPDHGRLSPPEAPDRPTISTASE  
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAPPRLSVEITGLEKGTSYKFRV  
 RALNMLGESEPSAPSRPYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNNT  
 PIHGFYIYYRPTSDNDSDYKKDMVEGDKYWHISHLQPETSYDIKMQCFNEGGESEFSNVM  
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTMAMVARSSDPLYLIVGVVLGSIVL  
 IIVTFIPFCLWRAWSKQKHTTDLGFPRLPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCPAAVGYPGMKPQQHCPGELQQQSDTSSLRQTHLGNGYDPQSHQITRGPK  
 SSPDEGSFLYTLPPDDSTHQLQPHHDCCQRQEOPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
 PPCCLGLVPVEEVDSRSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

## FIGURE 37

CGGGAGGCTGGTCGTATGATCCGGACCCATTGTCGGCCTCTGCCATGCCCTGCTCCTC  
 CCAGGCTCCCGCGGCCGACCCCCCGCGCAAC**ATG**CAGCCCACGGGCCCGAGGGTTCCCGCG  
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGAGACCACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGCTCCCC  
 AGCCTCTTACCAACGCCGGGTGCCCCAGCGCCCTCACTACCCCAGGCCTCACTACGCCAGG  
 CACCCCCAAAACCTGGACCTCGGGTCGCGCGAGGCCCTGATGCGGAGTTCCACTCG  
 TGGACGGCCACAATGACCTGCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
 TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCTCCTACTCTGAACCTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTAAAAGCTGGCCTGCCTCATGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCGCAGTTCTATGTGCTGGGGTGCCT  
 ACCTGACACTTACCTCACCTGCAGTACACCATGGCAGAGAGTTCCACCAAGTTCAGACAC  
 CACATGTACACCAACGTCAAGCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGCATGATGATAGATTGTCCTATGCATCGGACACCTGATAAGAAGGGCCTGG  
 AAGTGTCTCAGGCTCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG  
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATGTGATGGTACACT  
 GTCCATGGGGTGCAGTGCACCTGCTGCTAACGTGTCCACTGTGGCAGATCACTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGATTGGTGGAAATTATGACGGACT  
 GGCGGTTCCCTCAGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTCAAGGTGTCTCGTGGAAACCTGCTGCCGGTCT  
 TCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT  
 CCATATGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCTCAGAATGGACACCAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGTCCCTGGAGGTCTCAAATGCCT  
 CCCATACCTGTTCCAGGCCTGTGGCTGCCACCATCCACCTCACCCAGTGGCTC  
 TG**TGA**CACAGTCGGTCCCCGAGAGTCAGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

## **FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIGHRCASYSELELVSAEGLNSS
QKLACLVGXGGHSLDSSLVLSFYVLGVRYLTLCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKREESRAQSPVEAEFPYQQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

## FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCGGCTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**  
 AAGCTCTTATCTTGGTGGCTGTGGTGGGTGTTGCTGGTCCCCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGCACA  
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCAGGCCA  
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCAACCATTCAAGGTATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCCTGATGCTGGTGGACCCCTGTATGCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCATCCCTCGG  
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAAGGTGCCAGCAGCGGTGGAAGCTGC  
 AGGTGCAGGAGCAGCGGAAGACAGTCCTCGATCGGCACAAGATGCTCAGC**TAG**ATGGCCTGG  
 TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTTCCCTCGTTCCAGTCTCCCTTAAAGCCTGTGGCATTTCCTCCTT  
 CTCCCTAACCTTAGAAATGTTGACTTGGCTATTTGATTAGGAAAGAGGGATGTGGCTCT  
 GATCTCTGTTGCTTCTTGGGCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTGAGGCAGGCTCAGGAGTGGATGCGATCTGCTCTCCTGGCTCCACTCTG  
 CCGCCTTCCAGCTCTGAGTCTGGGAATGTTGTTACCCCTGGAAAGATAAGCTGGTCTTCA  
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTCACTGAGTGTGTTCTTCAGTG  
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCACTGGGTCTTCAGGGTGCAGTGG  
 AGCTGGTGGTTCGCTGCCCCCTGTGCACCTCGCACTGGGGCATGGAGTGCCATGCATACT  
 CTGCTGCCGGTCCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCTCCTCCCCAGTGTG  
 CACAGTCAGTGCAGGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCACAGCCCCCTGTACTTGGGTTGCCTCTGTCCCTGAACCTCGTTGTAACAGTGCATGG  
 GAGAAAATTTGTCCCTTGTCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAAATTG  
 TTTTATTTCTCTCA

## **FIGURE 40**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHLYNQNVSQKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYEERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

## **FIGURE 41**

## **FIGURE 42**

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN  
GICIPVTEILTPIPALDGTRHDRNIGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

### Signal peptide:

amino acids 1-25

## FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTGGCCTCCAAA  
 GTGTTGGGATTACAGGCAGTGGCCACCGCGCCGGCAACATCACGTTTAAAGGAAATTGATT  
 TCTTCAAATTATGGCAAATATTCCCTTCACTTATGTCAGAATGAGGAAGGA  
 TAGCTGCATTATTCAGTTTCATTGCATAGTAATATTCATGTAGTATTTCTAAG  
 TTATATTTAGTAATTATGTTAGATTATAGGTTAACATACTTGTGAAAATACTTG  
ATGTGTTTAAAGCCTGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTATCCCCCT  
 TTTAAAGTCATCCGTCCTGGCTCAGGATTGGAGAGCTTCGACCACCAAAATGGCAAACA  
 TCACCAGCTCCCAGATTTGGACCAGTTGAAAGCTCCGAGTTGGCCAGTTACCAACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCCCTACAACACTACTTCTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTTCAAATCTAACCTGAGCCATCCC  
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCCT  
 CCTGGTTGGAGTCCTTCCTCCAGGAAAATTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTGCAGCTCCAGCACGACCATTGAAAATATCTGTGTCTG  
 TCCACCAGCCACAGCCAAACACATCAAACACTTGTAAAGCGGCGGATACCCCCAGCTTCTAAG  
 ATCCCAGCTCTGCAGTGGAAATGCCTGGTTCAGCAGATGTACAGGATTAAATGTGCAGTT  
 TGGGGCTCTGGAATTGGGTCAAACCTCTCTCTGAATTGGATCAGCTCAAAGCAGTG  
 AAAATAGTAATCAGATTCCATCAGCTGTATTGAAAGTCTTAAGTGAGCCTTGAATACA  
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTATTACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCATAACAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
 GGAACCACATCATGAATGGACATGGTGGTGGTCAAAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTGTATGGCTGGTGCACCAACACAGAGGAAGAGGATAGCTCACGTGA  
 TGTGGAAAACACCAAGTTGGTCAATGGCTCATTGTTAAAAGCAGCCCTTGCTTTGT  
 TTTGGACCAGGTGTTGGCTGTGGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTCTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATAAGTATGCAT  
 TTTAAAGATGCTTGGCCAGGCGGGTGGCTGATGCCATAATCCAGTGCTTGGGGGCC  
 AAGGCAGGCAAGTGCCTAAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC  
 TGTCTCTACTAAATACGAAAAACTAGCCGGGTGTGGTGGCGCGCGTGCCTGTAATCCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTGGCTACAAAGTGAAGACTCC  
 GTCTGAAAAGA

## **FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQQPQPKHIKLA  
KRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASP  
VAMSSSYDQSSVHNRIPYQSPVSSSESAP  
GTIMNGHGGGRSQQTLDKYSSKLLSWLVPTKQRKRIA  
HVMWKT  
PVGQWLIR

**Signal peptide:**

amino acids 1-24

## **FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGCTGGCGGGGCC **ATG** GCGCTGCCATCCGAATCCTGCT  
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 AC CGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCCGCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGCAGCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTAACAGGTGGTGCACGGGACCGGCAGCCGCCGGG  
 GTCCCGCACGACCGCGCGACCGCCTGCTGGACCTCTACCGTGGCGAGCGCCGCCCTA  
 CGGGCCCTTTTCTGCGCACC CGCGTGGCTGTGGCGCGGATGCCTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCCACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCAATTACTGTGGCCTGCACGAACGCCGCTTCCACCTGACGGTCGCCAACCCACGC  
 GGAGCCGCCCGGGCTCTCCGGGCAACGGCTCCAGGCCACAGCGGCCAGGAGCCAG  
 ACCCCACACTGGCGCGGCCACAACGTCAATGTCATCGTCCCCGAGAGCCGAGCCCAC  
 TTCTCCAGCAGCTGGCTACGTGCTGGCACGCTGCTGCTCTCATCCTGCTACTGGTCAC  
 TGTCCCTGGCCGCCGCAGCGCCGGAGGCTACGAATACTCGGACCAGAAGTCGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTGCGCTGTGGCTGCAGGGGACCAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCCACAGCCCCCTGCCAGCTGCCAACGACCTAGACAAAGGTTCCGGAGGAGAACT  
 GCAAAT**AG**GGAGGCCCTGGCTCCTGGCTGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGCATCTCCTGATGCTCCGGGCTCACCCCCCTTCCAGCGGCTGGTCCCCTTCC  
 GGAATTTGGCTGGCGTATGCAGAGGCCGCCTCCACACCCCTCCCCAGGGCTTGGTGGC  
 AGCATAGCCCCCACCCCTGCCCTTGCTCACGGGTGGCCCTGCCACCCCTGGCACACC  
 AAAATCCCAGTGCATGCCCATCATGCCCTCAGACCCCTCTGGCTCTGCCGCTGGGGCTG  
 AAGACATTCTGGAGGACACTCCCAGAACCTGGCAGCCCCAAACTGGGTGAGCCTCA  
 GGGCAGGAGTCCCACCTCCAGGGCTCTGCTCGTCCGGGCTGGAGATGTTCTGGAGGA  
 GGACACTCCCAGAACACTGGCAGCCTTGAAAGTTGGGTGAGCCTCGGCAGGAGTCCCAC  
 CCTCCTGGGTGCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTGAATGCCAGCCCTGCTCCTGTGTTG  
 CTTGGGCCACCTGGGCTGCACCCCCCTGCCCTTCTGCCCCATCCCTACCCCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC  
 GGACTCTGCCCTGGCTGGAGTCTAGGGCTGGGCTACATTGGCTCTGTACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTGGGCTGTGTTGCCACTCTCAGCACCCACATT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGTCCCCATCTGATTTAAAAAAA  
 AAAAA

## **FIGURE 46**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLA VARGAPALLTCVNRGHVWTDRHVEEAQQVVHWDRQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADA FERGDFSLRIEPELEVADEGTYSCHLHHHYCGLHERRVF
HLTVAE PHAE PPPRGSPGNGSSHSGAPGPDTLARGHNINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGDVNLA EFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK
```

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGGGCGTGGCGCAGCGCGAC **ATGGCCGTTGTCTCAGAGGACGACTTT**  
 CAGCACAGTCAAACCTCACCGAACACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAGCTGCTGGACCGCCGCCCTGGCCTGCAGAGGCCAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTCAGCCTGGCATTGGCAGTCTACTGCCATGGAACCTCTT  
 ATCACTGCCAAGGGAGTACTGGATGTTCAAACACTCCGCAACTCCTCCAGGCCAGCCACGGGA  
 GGACCCCTGAGGGCTCAGACATCCTGAACACTACTTGAGAGCTACCTGCCGTTGCCCTCACCG  
 TGCCCTCCATGCTGTGCCCTGGCAACTTCCCTGCTTGTCAACAGGGTGCAGTCCACATC  
 CGTGCCTGCCACTGACGGTCATCCTGGCATCTTGTGATAACTGCACGGTGA  
 GGTGGACACTCCTCCTGGACCCGTGGTTTTGCGGTCACCATTGTCTGCATGGTATCC  
 TCAGCGGTGCCCTCACGTCTCAGCAGCAGCATCTACGGCATGACCGCTCCTTCCATG  
 AGGAACCTCCAAGCAGTATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCCATGACGG  
 CCACCATCTCCTCGTCTGCATGGACTCTACCTGCTGCTCCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCCTGTTCTGCCCATGTGTTCTGGTGAAGAGGAGCTCCCCA  
 GGACTCCCTCAGTGCCCTTCGGTGGCCTCCAGATTGATTCCCACACACCCCTCTCC  
 GCCCCATCCTGAAGAAGACGGCCAGCCTGGCTCTGTGTCACCTACGTCTTCCATCACC  
 AGCCTCATCTACCCGCCGTGCACCAACATCGAGTCCCTCAACAAGGGCTGGGCTCACT  
 GTGGACCACCAAGTTTTCATCCCCCTCACTACCTTCCCTGTACAACATTGCTGACCTAT  
 GTGCCGGCAGCTACCGCCTGGATCCAGGTGCCAGGGCCAAACAGCAAGGGCTCCAGGG  
 TTCGTGCTCCCTCGGACCTGCCTCATCCCCCTCTCGTCTGTAACTACCAGCCCCGGT  
 CCACCTGAAGACTGTGGCTTCCAGTCCGATGTGTAACCTCCTCAGCTCCCTGCTGG  
 GGCTCAGCAACGGTACCTCAGCACCCCTGGCCCTCTACGGGCTTAAGATTGTGCCAGG  
 GAGCTGGCTGAGGCCACGGAGTGGTGTGCTTTATGTGCTTGGGCTTAACACTGGG  
 CTCAGCCTGCTTACCCCTGGTGCACCTCATC **TAGAAGGGAGGACACAAGGACATTGGT**  
 CTTCAGAGCCTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC  
 TAAAGTTTCACTGGGGACAGAGAGCAGAGCACACTCGGGCTCATCCCTCCAAGATGCCA  
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATCCAGTCATATTAAACAGAACACT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAATCAGGGTACTCCCTCACAGCTGATGGTTA  
 ACATTCCACCTTCTTCTAGCCCTCAAAGATGCTGCCAGTGTGCTGCCCTAGAGTTATTACA  
 AAGCCAGTGCCAAAACCCAGCCATGGCTCTTGCAACCTCCAGTGCCTCATCCAGCT  
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTACCCCTGAAGGGTCTCCCTGGAATGGA  
 AGTCCCTGGCATGGTCAGTCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
 GCGGGTGAACAACAGCCACTAACCAAGAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT  
 GCTTCATTCCAGAGGGGACCAAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCGGCCTGGG  
 TTTCAAAAAAAAGAGGGATCCTCATGACCTGGTGGTATGGCCTGGTCAAGATGAGGGTC  
 TTTCAGTGTCTGTTACAACATGTCAAAGCCATTGGTCAAGGGCGTAATAAAACTTGC  
 GTATTCAAAAA

## **FIGURE 48**

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFSLGI  
GSLLPWNFFITAKEYWMFKLRNSSLSPATGEDPEGSDILNYFESYLA  
VASTVPSMLCLVANFL  
LVNRVAVHIRVLASLT  
VILAIFMVITALV  
KVDTSSWTRGFFAVTIVCMV  
ILSGASTVF  
SSSI  
YGMTGSFPMRNSQALISGGAMGGTV  
SAV  
ASLVDLA  
ASSDVRNS  
ALAFFLT  
ATIFLVLCMGLY  
LLL  
SRLEYARYM  
RPV  
LA  
AHV  
FSG  
EEE  
LPQ  
DSLS  
APS  
VAS  
RFID  
SHT  
PPL  
RPI  
LKKT  
ASL  
G  
CVTYVFFITSLI  
YPAV  
CTN  
IES  
LNKG  
G  
SL  
WTT  
KFFI  
PLTT  
FL  
LYN  
FAD  
LCR  
Q  
LTAWI  
QVP  
GPNS  
K  
AL  
PGF  
V  
LL  
RT  
CL  
I  
PL  
F  
V  
LC  
NY  
Q  
PRV  
HL  
K  
TV  
V  
F  
Q  
SD  
V  
P  
A  
L  
L  
S  
L  
G  
L  
S  
N  
G  
Y  
L  
S  
T  
L  
A  
L  
Y  
G  
P  
K  
I  
V  
P  
R  
E  
L  
A  
E  
A  
T  
G  
V  
V  
M  
S  
F  
Y  
V  
C  
L  
G  
L  
T  
L  
G  
S  
A  
C  
S  
T  
L  
L  
V  
H  
L  
I

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330, 448-472

## FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA  
 TCTCCCACCGAGAGTC**ATG**CCCCATTGGCCCTGCACCTCCTCGCCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCC  
 GAAGCCCCAGAGGGTATTGTGGTTGGCGCTGGTGTGGCCGGCTGGTGGCCGCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATGGGGCCGCATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGAGCTGGAGGCCATGCGCATGCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGCTCAACCTGACCAAGTTCACCC  
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGAG  
 AAGGTGCCCGAGAAGCTGGCTACGCCCTGCGTCCCCAGGAAAAGGGCCACTGCCCGAAGA  
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGCTGCAGAAAGG  
 CGATGAAGAAGTTGAAAGGCACACGCTCTTGAATATCTTCTGGGGAGGGAACCTGAGC  
 CGGCCGGCCGTGCAGCTCTGGAGACGTGATGTCGAGGATGGCTTCTTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGCCACAGCTGCCCTCAGCAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGACCTGCTGCCCGCGCGCTGCTGAGCTCGCTGTCCGGGTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCACGTGGCTGCTGACGGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTCTGCCCGCTGCCGACATGCAGGAGGCGCTGCCAGG  
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTCCGAGGCCCTCTGGCGCGAGGA  
 GCACATTGAAGGCCGAACTCAAACACCGATGCCCGTCGCGCATGATTTCTACCGCCGC  
 CGCGCGAGGGCGCGCTGCTGGCCTCGTACACGTGGTGGACGCCGGCGAGCGTTCGCC  
 GGCTTGAGGCCGGAAAGAGGCCTTGGTACAGCCGCCGCGCTGCAAGCGTTGGCGGAGGAC  
 TGCGTGCGCCAGCTCTGGACGGCACCGCGCTCGTCAAGCGTTGGCGGAGGAC  
 GCCAGGGTGGCTTGTGGTACAGCCGCCGCGCTGCAAGCGAAACCGAAAAGGATGACTGGAC  
 GTCCCTTATGCCGCATCTACTTGCCTGGCGAGCACACGCCCTACCCGCACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGGCGCTGCCCGCCATCAAGATCAACAGCCGGAAAGGGCCTGCAT  
 CGGACACGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGG  
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG  
 CCAGTTATCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTCGGAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 50**

MAPLALHLLVLVPIISSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSAGHKVTILEADNRIGGIFTYRDQNTGWIGELGAMRMPSSHRIIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPPEKLGYALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLNSRPAVQLLGDVMSEDGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL  
KVLKADVVLLTASGPRAVKRITFSPPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

## FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGCCCTCTGCCTGC**AT**  
**GGACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACCAAGCAGCGAGGGAAAGGACAGGGACTCGTGTGGCAGGAA**  
 GAACTCAGAGCCGGAAAGCCCCCATTCACTAGAACGACTGAGAGATGGGCCCCCTCGCAGGGCTGATATTCCCT  
 GCTGCTGTTACAAAGATGCTTTTATCTTAACCTTTGTTCCCCACTTCCGACCCGGCGTTGATCTGCAT  
 CCTGACATTTGGAGCTGCCATCTTCTGTGGCTGATCACAGACCTCAACCGCTTACCTCTTGACCTGAA  
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCACCGAAGGGGTTCCAGAAGAACAACTAACAGTTGCTG  
 CTTCTAGATGCCAAGACTATGTATGAGGTTTCCAAGAGGACTCGCTGTGACAAATGGGCCCTGCTTGGG  
 ATATAGAAAACCAACCAGCCCTACAGATGGCTATCTTACAAACAGGGTGTGATAGAGCAGAGTACCTGGGTT  
 CTGTCCTTGCAAAAGGTTATAAATCATCACAGACCTGAGGAGGAGCACCGTACAGTGGTAGCTGACAAATAGGCCAGAGT  
 GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGACCTCTGTATGACACCTTGGGACCAGAAC  
 CATCGTACATATTGTCAACAAGGCTGATATGCCATGGTGTGACACACCCCCAAAAGGCATTGGTGTGAT  
 AGGGATGTAGAGAAAGGCTCACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTIGATGATGACCTGAA  
 GCAAAGAGGGAGAAGAGTGGATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTCAG  
 AAAACCTGTGCCCTCCTAGCCAGAACCTGAGCGTCACTGCTTCAACAGTGGGACCACAGGTGACCCCAAAGG  
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCTGCCCTCTCAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCCTGATGATGTGGCATATCCTACCTCCCTGGCTCATATGTTGAGAGGATTGTACAGGCTGTTGTGTA  
 CAGCTGTGGAGCCACAGTGGATTCTTCAAGGGATATTGGTGTGAGCACATGAAAGACTTGAAGCC  
 CACATTGTTCCCGCGGTGCCTCGACTCCTAACAGGATCTACGATAAGGTACAAAATGAGGCAAAGACACCC  
 GAAGAAGTTCTGTGAAGCTGGCTGTTCCAGTAAATTCAAAGAGCTTCAAAAGGTTATCATCAGGCATGATAG  
 TTTCTGGACAAGCTCATTTGCAAAGATCCAGGACAGCCTGGCGGAAGGGTCTGTGTAATTGTCACTGGAGC  
 TGCCCCCATGTCACACTTCAGTCATGACATTCTCCGGGCAGCAATGGGATGTCAAGGTGATGAAGCTTATGGTCA  
 AACAGAATGCAAGGTGGTGTACATTACATTACCTGGGACTGGACATCAGGTACAGTGGGGTGCCTGG  
 TTGCAATTACGTGAAGCTGGAAAGATGTGGTGTACATTACCTGGGACTGGACATCAGGTACAGTGGGGTGCCTGG  
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCCTGAGAAGAACACAGGAAGGCCCTGACACTGATGGCTG  
 GCTTCACACAGGAGACATTGGTCGCTGGCTCCGAATGGAACACTCTGAAGATCATCGACCGTAAAAAGAACATT  
 CAAGCTGGCCAAGGAGAACATTCGACCAAGAGAACATGAAAGAACATTTCTACAAACAGGAGTCAACCAGTGTACA  
 AATTGTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGTGACACAGATGTACTCC  
 ATTTGCAAGCTGGGACTGGGCTCCTTGAGGAACCTGTGCAAAACCAAGTTGTAAGGGAAAGCCATT  
 AGAAGACTTGCAAGAAATTGGGAAAGAAAGTGGCTTAAACTTTGAAACAGGTCAAAGCCATTTCATCC  
 AGAGCCATTTCATTGAAAATGGGTCTTGACACCAACATTGAAAGCAAAGCAGGGAGAGCTTCCAATACCT  
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGCCACTG  
 TGCACTGCTTGTGAGAAAATGGATTAAAATCTTACATTGTTGCCTTCCCTATTGTTTAACC  
 TGTAAACTCTAAAGCCATAGCTTGTATTGAGACATATAATGTGTAACACTTACTGCTCCAAATAATCA  
 ATCCGTCTTCCCCTTCATCTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTATCAACATGCCTGCTTCAA  
 GATCCCAGTTATGTTCTGTGCTCTCATGATTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT  
 CAAAGGGACCCCTGTGCCCTCTTGTGATAAACATAACTTGCAACAGTCTCTATGCTTATTACA  
 TCTTCTACTGTTCAAACAAAGAGATTAAATCTGAAAAACTGCTACAATTGATGTTCTAGCCACTCCAC  
 AAACCACTAAATTTAGTTAGCCTACTCATGTCATGATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
 CTGCGTAAATTAAATGTTGACTGAAGGGAAAAGTTGATCATACCAACATTCTCAAACCTCTAGTTAGATA  
 TCTGACTTGGGAGTATTAAGGCTATGACACTGTCCAAAAGGAATGCTGTTCTAAAGCATTATT  
 CAGTAGGAACCTGGGAGTAAATCTGTTCCCTACAGTTGCTGAGCTGGAAGCTGTGGGGAGAGTTGACA  
 GGTGGGCCAGTGAACACTTCCAGTAAATGAAGCAAGCAACTGAAATAAAACCTCTGAACGGAAACAAAGATCT  
 ACAGGCAAGCAAGATGCCACACAAACAGGCTTATTCTGTGAAAGGAACCAACTGATCTCCCCCACCCTGGATT  
 AGAGCTCTGCTTACCTTACCCACAGATAACACATGTTGTTCTACTGTAAATGTAAGTCTTAAAATAAAC  
 TATTACAGATAAAAAAA

**FIGURE 52**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSSLKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSAAAFLKCVEHAYEPTPDDVAISYLPALAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPRLLNRYDKVQNEAKTPLKKFLLKLA
VSSKFKELOQGIIRHDSFWDKLIFAKIQDSLGGRRVRVIVTGAAPMSTSVMFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVGPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPKETQEAQDSDGWLHTGDIGRWLPGNTLKIIDRKKNIFKLAQGEYIAPEKIEINIYNR
SQPVLQIFVHGESLRSSLVGVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIIFLHPEPFSIENGLLPTLKAKRGELSKYFRTQIDSPLYEHIQD

```

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

## FIGURE 53

GGAGGC GGAGGCCGCGCGAGCCGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG  
 CCCGGGGCCCTAAGCCATTCTGAAGTCATGGCTGGCAGGACATTGGTACCCGCCAAT  
 CCGT **ATG** GACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTGGGCTCGGAAGAACGG  
 AGCTGGTACCTTACCTGGAAGTATAAAGTACGACAAACCAGCGGGCCCTCGGGAGATTCTGTCA  
 GACAGGGGCCGTGCTTCTGCTGGTACTGTCAATTGTCAATATCAAGTTGATCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
 CTAGGCCGCTGGAGCCCCACGGCGAGAGGAGTGGCAGTGGATGGCACCGTGCTGGAGGATG  
 GGTGTATTCAAGTCGAGCAAAGTATATGTGGCAGTGGATGGCACCGTGCTGGAGGATG  
 AGGCCCGGGAGCAGGGCCGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGCACGTG  
 ATGGCAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTATTCT  
 CAACATGGTAGCGCCCGGCCAGTGCTCATCTGCACTGTCAAGGATGAGGCCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGGAGGAGCCTGGCAGCCAGGCTGGCCTGCCCTGGC  
 TGGAGGGACACATGGCCTCTGTTGGAGCAGAAAAGGAGGTCTGTCTCGGGAGAAACATTC  
 TAAGTCACCTGCCCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGCG  
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA  
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCCGTGGCTGTCAATTGCA  
 GGAACCGACCCAAATTACCTGTACAGGATGCTGCCTCTGCTTCAGCCCAGGGGTGTCT  
 CCTCAGATGATAACAGTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT  
 GTTGGTCTGAGGGCATTCCAGCATACTCCCATCAGCATCAAGAATGCCCGGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTCAGTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTGCTGGAATGACCAGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCAGCCTGGCTGGCTGGGTGCTC  
 AGGAGGTCTGTACAAGGAGGAGCTTGAGGCCAAGTGGCTACACCGGAAAAGCTCTGG  
 TTGGGACATGTGGATGCGGATGCCTGAACAAACGCCGGGGCGAGAGTGCATCATCCCTGAC  
 TTTCCGATCCTACCACTTGGCATCGTCGGCTCAACATGAATGGCTACTTCACGAGGCC  
 TACTTCAAGAACGACAAGTTCAACACGGTTCCAGGTGTCCAGTCAGGAATGTGGACAGTCT  
 GAAGAAAGAACGTTATGAGTGGAGTTCACAGGGCTGTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCTTGTGAAGACTCTTCTGCCAGACACAGAGGCCACACCTACGTGGCC  
 TTTATTCGAATGGAGAAAGATGACTTCACCACCTGGACCCAGCTGCCAAGTGCCCTCCA  
 TATCTGGACCTGGATGTGCGTGGCAACCAGCCTGGGCTGTGGAGATTGTTGGAAAGAAGA  
 ACCACTTCCTGGTGGGGGCTCCGGCTCCCCCTACTCAGTGAAGAACGCCACCCCTCAGTC  
 ACCCCAATTTCTGGAGGCCACCCCAAAGGAGGAGGGAGGCCAGGAGGCCAGAACAGAC  
**ATG** GACCTCCTCCAGGACCCCTGCAGGGCTGGTACTGTGTACCCCCAGGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGCTGGGCTACCTGTTTAACA  
 TGAGACTTAATTACTAACCAAGGGAGGGTCCCTGCTCCAACACCCGTTCTGAGTT  
 AAAAGTCTATTACTTCTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG  
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCTCACTTCCAGGCCTGGCTCAGAAC  
 ACCTATTATTGACTGCTCTGAGGGCCTTGAAACAGGCCAACCTGGAGGGCTGGATTTC  
 TTTTGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTTACTCAGGAAACTGCTGTGCC  
 CAACCCATGGACAGGCCAGCTGGGCCACATGCTGACACAGACTCACTCAGAGACCCTA  
 GACACTGGACCAGGCCCTCTCAGCCTCTTTGTCCAGATTCCAAAGCTGGATAAGTT  
 GGTCAATTGATTAAGGAGAAGCCCTCTGGGAAAAA

**FIGURE 54**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPDRVLDVEVYSSRSKVVAVDGTIVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRLLLLFCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVVLEEDLDIAVDFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRCIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSLKKEAYEVEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVRGNH RGLWRLFRKKNH
FLVVGVVPASPVKKPPSVTPIFLEPPPKEEGAPGAPEQT

```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

## **FIGURE 55**

CGGACGCGTGGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACCTCTTGGAACCAACAC  
 CTGTTAAAGAACCTAACGACCACTTAAAGCCACTGGAAATTGTTGCTAGTGGTTGTGGGTGAATA  
 AAGGAGGGCAGA**ATGG**ATGATTCACTCATTAGCCTGCTGCTCTGGCTATGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTTGG  
 GTGCTGGCCTCTGTGGAACTGCTCTGGCAGTCATCGCCTGAAGGAGTACATGCCCTTATGAA  
 GATATTCTTGAGGGAAAACACCAAGCAACTGAAACACATAATGTGATTGCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCATATTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTCACTGTTGCTGGTGGACCAGATTGTAACCTCCATGTGCATTCT  
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACACGCTGGGCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTGGGAGCAGCAGCATCTACCTCACAGACCAGTGTCCAGTTAATTG  
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTGGACTGGTTCTTGCATTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAACGCCCTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTCTGCGGGACATTCTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGCGGA  
 ATAGGGCACAGCCACAAGCCGATGCCACGGGAGGGAGAGGCTCAGCCGCTGGAAAGTGGCAGCCCT  
 GGTTCTGGGTTGCCTCATCCCTCATCCGTCACTAGGACACCAGCAT**TAA**ATGTTCAAGGTCCAGC  
 CTTGGTCCAGGGCCGTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTCCCTAGTC  
 TCTTGTCTCACCTGCGCATCTACATGATTCTAGAGTCCAGAGGGAGGTGAGGTAAAACCTG  
 AGTAATGGAAAAGCTTTAGAGTAGAAACACATTACGTTGCAAGTTAGCTATAGACATCCCATTGTGT  
 TATCTTTAAAAGGCCCTGACATTTCGCTTTAATATTCTCTTAACCTATTCTCAGGGAAAGATG  
 GAATTTAGTTAAGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTGATTATGAAAATACAGT  
 GTTCTGTAATTAAAGCTATGTCCTTCTCTAGTTAGAGGCTCTGCTACTTTATCCATTGATTTT  
 AACATGGTTCCCACCAGTAAAGACTGGTGCTTAGCATCTATGCCACATGCGTTGATGGAAGGTATA  
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC  
 AAGACACATTGAAAGCTCTTTACTCAAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT  
 TAAACAGCTCCTTGGCACGTGCCCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGG  
 TGGGAGGAGCTCTAAAGAGGTGACTGGTATTTGTTAGCATTCTGTCAAGTTCTCCTTGCAGAAT  
 ACCTGTCTCCACATTCTAGAGAGGAGCCAAGTTCTAGTTCAAGTCTAGGCTTCTCAAGAA  
 CAGTCAGATCACAAAGTGTCTTGGAAATTAAAGGATATTAAATTTAAGTGAATTGGATGGTTAT  
 TGATATCTTGTAGCTTTAAAAGACTACCAAAATGATGGTGTCTTTTTGGATGGTT  
 TTTTTTTAATTATTCTCTAGCAGATCAGCAATCCCTCTAGGGACCTAAACTAGGTCACTT  
 GGCACACTGTGCTCTCACATAACCAACCTGTAGCAAGATGGATCATAATGAGAAGTGTGTC  
 TTGATTAAAGCTTATTGGAATCATGTCCTGTCTCTCGTCTTTCTTGTCTTCTAACTTT  
 TCCCTCTAGCCTCTCGCCACAATTGCTGCTACTGCTGGTGTAAATTGTGTTGGGATGAATT  
 CTTATCAGGACAACCACCTCTCGAACTGTAATAATGAAGATAATAATCTTTATTCTTATCCCCT  
 CAAAGAAATTACCTTGTGTCAAATGCCGTTGTTGAGCCCTAAACACACCTCATGTGAA  
 ATTGACACAATCACTAATCTGTAATTAAACAATTGAGATAGCAAAAGTGTAAACAGACTAGGATA  
 ATTTTTTTCATATTGCAAATTGAAACCTGTCTGTCAAATAAGTGTATAATTGTAT  
 TATTAATTATTCTTACCTCTACCAATTCTCAAACACATTACACTAAGGGGAAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGACGTAGTTGTAACAGCTTCTATGACGCATAAGCTAGCATGCCATAG  
 ATTTATTCTCATGAATTGTCAGGGATCAGCAGCTGTGAAATAAGCTTGTGAGCCCTGCT  
 GGCCACAGTGGAGGAAAGTAGCACAATAGGATACAGTTGTATGTTAGTCATTGGCAACAATTGCA  
 ATTTACTACCAAGAGAAGGTATAGTATGGAAAGTCAAATGACTTCCTGATTGGATGTTAACAGCT  
 GACTGGTGTGAGACTTGAGGTTCATCTAGTCCTCAAACACTATATGGTGCCTAGATTCTCTGGA  
 AACTGACTTTGTCAAATAAGCAGATTGTTAGTCAAAAAAA

## **FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVQDQ  
IGNSHVHSTDDPEAARSSNSKITTGLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLVFALAAPVMSMVTYLGSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLILSVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

## FIGURE 57

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGCCCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTAGCGCTGATTGAGATGATGGGCTTGG  
 GAAACGGCGTGCAGCATGAAGTCGCCGCCCTCGTGCCTGGCCGCCCTGGTGGCCTGCATC  
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCGGAGCGTGGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCGTGGAGCTGAAGA  
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCAGGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGTTTGGTGA  
 TAACATCACACAGGTGAGAGGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
 GGAATTACGGCAGGCAGGCTGCAGCAGGATGTCCTCCAGTTAGAAGAACAGACCAACCTGGAG  
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGGCTGTAGCTTCAGAGACCTGA  
 GTGAAAACAAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAAGGGAAACGTGCTTGGTAACAGCAA  
 GTCCCAGACACCAGCCCCAGTCCGAAGTGGTTTGGATTCAAAGAGACAAGTTGAGAAAG  
 AGGAAACCAATGAGATCCAGGTGGTAATGAGGAGCCTCAGAGGGACAGGCTGCCAGGAG  
 CCAGGCCGGAGCAGGTGGTAAGACAGACCTGTAGGTGGAAAGAGGGCTCGGGGGAGCCGG  
 AGAACTGGGCCAGACCCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGCTTGTCACTCCCGACGGACAGGAGGAGCAGGAAGCT  
 GCCGGGAAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGATGACAGAAACATAGATG  
 TTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTGAAAAGCGG  
 AATCATAACACTTGAATTGAACCTGGAATCACATATTCAACACAGGGCGAAGAGATGACTA  
 TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAATGTACATCTGA

## **FIGURE 58**

MMGLGNRGRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNNDQRQQLQALSEPQPRLQAAAGLPHTEVPGKGNVLGNSKSQTPAPSSEVVLDSKR  
QVEKEETNEIQVVNEEPQRDRLPQEKGREQVVEDRPVGGRGF GGAGELGQT P QVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEQEAAGEGRNQQKLRGEDDYNMDNEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

## FIGURE 59

GG**ATG**CAGAAAGCCTCAGTGGCTTCCCTGGCCTGGGCTGCTTCTTCTACGCTGGCATTGCCCTCTCA  
 CCATGGGCTTCTGCTACCCGTTGGAGCTACCAACCATAGCAGCTGCCAAGAGCCCCCAGGCCCTGGTCCC  
 TGCCATGGGGAGCCAAGGGAAACCTGGGCTGCTGGATGGCTTCCCGATTTGGGGGTGTGTTGGTGTGA  
 TAGATGCTCTGCGATTGACTTCGCCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCCGTCTCCCTACCCCT  
 TCCTGGCAAACTAAGCTCTTGCAAGGAGATCTGGAGATTAGCAGCCCCACCATGCCGGCTCTACCGATCTCAGG  
 TTGACCCCTCCTACCAACCACATGCAGGCCCTCAAGGCCCTCACCACTGGCTACTGCCTACCTTATTGATGCTG  
 GTAGTAACCTGCCAGCACGCCATGGAAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGCGTAG  
 TCTTCATGGGAGATGATACTGGAAAGACCTTTCCCTGGTCTTCTCAAAGCTTCTTCCATCCTTC  
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCTGGAACACCTCACCCACCATGGACAGTGGTAATGGG  
 ACGTGCTGATTGCTACTTCCTGGGTGTGGACACTGTGGCCACAAGCATGCCCTCACCAACCTGAAATGCCA  
 AGAAACTTAGCCAGATGGACCAAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG  
 CTGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGACAGTGGAGCTGGAGGTCTCAGCTGCTCTTTC  
 TGTATAGCCCCACAGCAGCTTCCCAGCACCCACAGAGGGAGCCAGAGGTGATTCTCAAGTTAGCCTGTG  
 CCACGCTGGCCCTGCTGGCTGGCATCCATTGGAATATCGGGAAAGTGTGAGCTTCTCAG  
 GGGTGAGGACTCCCAGCCCCACTCTCTGCTTAGCCAAGCCTCAGCTCTCATCTCAATGCTCAGCAGGTG  
 CCCGATTTCTCATACCTACTCAGCTGACTCAGGACCTCAAGCTAAGGAGCTTCAGCTGCAGAACCTCT  
 TCTCCAAGGCCCTCTGCTGACTACCAAGTGGCTTCTCCAGAGCCCCAAGGGGCTGAGGCAGACTGCCGACTGTGA  
 TTGCTGAGCTGCAGCAGTCTCTGGCTGGCCATGTGCATCGAGTCTGGGCTCGTTCTCTGGTCC  
 GCATGGGGGGGTACTGCTCTTGGCTGCTTCTGTTATCTGCTGCTGGCATCTCAGTGGCAATATCCC  
 CAGGCTTCCATTCTGCCCTACTCTGACACCTGTGGCCTGGGCTGGTTGGGCCATAGCGTATGCTGGAC  
 TCCTGGGAACTATTGAGCTGAAGCTAGATCTAGTGGCTCTAGGGCTGTGGCTGAGCTCATTCTCCCTT  
 TTCTGTGGAAAGCCTGGGCTGGCTGGGCTTCCAAAGAGGCCCTGGCAACCCCTGTTCCATCCCTGGGCCGTCC  
 TGTTACTCCTGCTGTTGCTTGGCTGTTCTCTGATAGTTGGTAGCTGAGGCCAGGGCACCCCT  
 TCCTTTGGGCTCATTCTGCTCTGGTGTCCAGCTCAGTGGGAGGCCAGTGTCTCCACCTAACGCTAC  
 TCACAAATGCCCGCCCTGGCACTTCAGCCACAACAAACACCCCCACGGCACAATGGCATATGCCCTGAGGCTTG  
 GAATTGGGTTGCTTTATGTACAAGGCTAGCTGGCTTTTCTAGCTGGCCTGAGGACACCTGTTGCCACT  
 CCTCTCCCTGGCTGAGCTCTGGCATCCATGGTGGTGGCGAGCCAAGAAATTATGGTATGGAGCTTGTGG  
 CGGGCCTGGTGGCCCTGTTAGCTGCCGTGCGCTGTGGCTCGCCGCTATGGTATCTCAAGAGCCCCGAGCCAC  
 CCATGCTCTTGTGCGTGGGACTGCCCTAATGGCATGGTACTGCTGCCTACTGGCATTGGCTGGGG  
 CAGATGAGGCTCCCCCGCTCCGGCTCTGGCTCTGGGCAATCCATGGTGTGCTCGGCTGTAGCAGGGC  
 TGGCTGCTCAGGGCTCGCGTGTGCTCTGGAAAGCCTGTGACAGTGTGGTAAGGCTGGGAGGCCCTCAA  
 GGACCAAGGACTGTCTCACTCCCTCTCAGGCCCCCCTACTCTCAAGCTGACTGGATTATGTGCTCCCTCAA  
 TCTACCGACACATGCAGGAGGTTGGGGCCGGTTAGAGAGGACCAAATCTCAGGGCTCCCTGACTGTGGCTG  
 CTTATCAGTTGGGAGTGTACTCAGCTGCTATGGTACAGCCCTCACCCCTGTGGCCTTCCACTCTGCTGT  
 TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTCTGTTCTGAGAGCTTCTCTACATCTGCTGCTG  
 CTGGGATACCCGTACCAACCCCTGGCTTACTGTGCCATGGCAGGACTCTGGCTTGGCCCTCATGGCA  
 CACAGACCTCTACTCCACAGGCCACCCAGCTCTTCCAGCCATCATTGGCATGCAGCCTCGTGGGATTCC  
 CAGAGGGTATGGCTCTGACTTGGCTGCTGCTTGTACTGGAGCCAACACCTTGGCTCCACCTCCT  
 TTGCGAGTAGGTTGCCACTGCTCTGCTCTGGCTTCTGTGAGAGTCAAGGGCTGCCAGAGACAGCAGC  
 CCCAGGGAAATGAAGCTGAGGCCAGAGTCAAGACCCGAGGAGGAAGAGGAGGCCACTGATGGAGATGCCGCTCCGG  
 ATGCGCCTCAGCACTCTATGCAGCACTGAGCTGGGCTCAAGTACCTTATCTGGTATTCTGAGATT  
 TGGCCTGTGCCCTGGCAGGCCATCCTCGCAGGCATCTCATGGTCTGGAAAGTGTGCTTGGCTTAAAGTTCATAT  
 TTGAGGCTGTGGCTTCATTGTGAGCAGCGTGGGACTTCTCTGGCATAGCTTGGTGTGAGAGTGGATGGTG  
 CTGTGAGCTCTGGTTCAGGCAGCTATTCTGGCCAGCAGAGG**TAG**CCTAGTGTGATTACTGGCATTGGCT  
 ACAGAGAGTGTGGAGAACAGTGTAGGCCAGGGCTGACAGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC  
 TCTTACTATCATGCAGCCAGGGCCGCTGACATCTAGGACTTCATTCTATAATTCAAGGACCAAGTGGAGTA  
 TGATCCCTAACTCCTGATTGGATGCATCTGAGGGACAAGGGGGCGGTCTCGAAGTGGAAATAAAATAGGCCGG  
 GCGTGGTGACTIONCACCTATAATCCCAGCACTTGGGAGGCCAGAGGTGGAGGATTGCTTGGTCCAGGAGTTCA  
 AGACCAGCCTGTGGAACATAACAAGACCCGCTCTACTATTAAAAAAAGTGTAAATAAAATGATAATAT

**FIGURE 60**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLTRLELTNHSSCQEPPPGPSLPWGSQGKPGACW
MASRFSRVVVLVLIDALRFDFAQPQHSHVPREPPVSLPFLGKLSSIQRILEIQPHHARLYRSQ
VDPPTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDLTVNGILEHLYPTMDSGEWDLIAHFLGVDHCGHKHGPHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAAGWGSKRPLATLFPIPGPVLLLLFRLA
VFFSDSFVVAEARATPFLLGSFILLVVQLHWEGQLLPPKLLTMRPLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLQSF
LLHLLAAGIPVTPGPFTVPWQAVSAWALMATQTFYSTGHQPVPAIHWHAAFVGFPAGEHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFILGIQILACALAASILRRHLMVWKVFAPKFI FEAVG
FIVSSVGLLGIALVMRVDGAVSSWFRQLFLAQQR

```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

## FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGCGCCTGGGGACGGGCAGTCCCTGT  
 GTCTCTGGTTGCCTAAACCTGCAAACATCACCTCTTATCCATCAACATGAAGA**ATGT**  
 CCTACAATGGACTCCACCAGAGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCGTTGT  
 CCTGACAGCTCCAGAGAAGTGGAAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGTGACCAACCACACGCTGGTGTACCTGGCTGGAGCCAACACTCTTACTGCGT  
 ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG  
 CCAGGACTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTCTGGTATGTTTG  
 CCCATATCTATTACCGTGTCTTTCTGTGATGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAATTGATTTGATTATGAAATGAATTGACAAAA  
 GATTCTTGTGCCTGCTGAAAAAATCGGATTAACTTATCACCTCAATATCTGGATGAT  
 TCTAAAATTCTCATCAGGATATGAGTTACTGGGAAAAGCAGTGATGTATCCAGCCTAA  
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCTCAGGAGGAAGAGGGAGGTGAAACATTAG  
 GGTATGCTTCGCATTGATGGAAATTTTGACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCTCAGCAGAACAAATACCCCCGATAAAACAGTCATTGAATATGA  
 ATATGATGTCAGAACCACTGACATTGTCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGGCCG  
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGATCCCC  
 AACTGGCAGGCTGTATTCCCTCGCTGTCCAGCTCGACCAGGATTCAAGGGCTGCGAG  
 CCTTCTGAGGGGATGGCTCGAGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTATGGAGGAATGGGGT  
 TATATGTGCAGATGGAAA**TGA**TGCCAACACTCCTTGCCTTGTTCCTGTGCAAAC  
 AAGTGAGTCACCCCTTGATCCCAGCCATAAAGTACCTGGATGAAAGAAGTTTTCCAGT  
 TTGTCAGTGTCTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTG  
 GTTCATGCATGTAGGTCTTTAACATGATGGTGGCCTCTGGAGTCCAGGGCTGGCCGGT  
 TGTTCTATGCAGAGAAAGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTACAGG  
 TGGGTGT

## **FIGURE 62**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQQRVFKEKLKLLTLCISIQQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLWLEPNTLYCVHVESFVPGPPRRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILIGNEFD
KRFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEDVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGGLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQMN
```

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## FIGURE 63

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGTCTCTGCAGGGAGACGCCAGCCTGCG  
 TCTGCC**ATG**GGGCTCGGTTGAGGGCTGGGACGTCTGCTGACTGTGCCACGCCCT  
 GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATGGGGGCCACGAGG  
 TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTCGGGGCCAACATCACTGCGGA  
 GGCTTCCTGCTGCGAGCCCCTGGGTGGTCTCGGCCGCCCAGTCTCAGGCCACAGAGACCT  
 CCGCACTGGCCTGGTGGTCTGGCGCCACGTCTGAGTACTGCGGAGCCCACCCAGCAGG  
 TGTTTGGCATCGATGCTCTCACACGCACCCGACTACCACCCATGACCCACGCCAACGAC  
 ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGCTGCTGAGGCT  
 GCCAGGGAGAAGGGCCAGGCCACAGCCCCACAGCGGGACACGGTGCCGGTGGCTGGCTGGGCT  
 TCGTGTCTGACTTTGAGGAGCTGCCGCTGGACTGATGGAGGCCAAGGTCCGAGTGCCTGGAC  
 CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGAG  
 TGGGGACAGCCACAGACGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA  
 ACCGGGCTCACGGCCTCGTTCTCGGGCCTCTGGTGCGGCAGCCCAAGACCCCGAC  
 GTGTACACGCAGGTGTCGCCCTTGTGGCCTGGATCTGGGACGTGGTCGGAGCAGTCC  
 CCAGCCCCGGCCCTGCCTGGACCACCAGGCCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT  
 TGCAGGATGCAAATGAGATGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCACGGG  
 AAGCCTGATGTTCAAGGTTGGGTGGGACGGGAGCGGTGGGCACACCCATTCCACATGCA  
 AAGGGCAGAAGCAAACCCAGTAAATGTTAACTGACAAAAAAAAAAAAAGAAA

a. If the sequence ends in a T, then the next sequence is the same as the previous sequence. If the sequence ends in a G, then the next sequence is the same as the previous sequence. If the sequence ends in a C, then the next sequence is the same as the previous sequence. If the sequence ends in a A, then the next sequence is the same as the previous sequence.

## **FIGURE 64**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVF
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

**Signal peptide:**

amino acids 1-30

## FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCACTCCGGACGCCCTGACGCCCTGA  
 CGCCTGTCCCCGGCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGACCGGTAG  
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGCTTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTGACGGCGCCAACACAGGCATGGGAAGCAGACCGCCTT  
 GGAACCTGGCCAGGAGAGGAGGAAACATCATCCTGGCCTGCCAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCTACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTGGCGTTAACCAACCTGGTCACTTCTCTTGACAAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCATGTTGCTGG  
 GCACATAGACTTGTACGACTTGAACACTGGCAGACAGGAGAAGTATAACACCAAAGCCGCC  
 ACTGCAGAGCAAGCTCGCCATCGCCTCTCACCAAGGAGCTGAGCCGGCGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCCAGGACAGAGCTGGGAGACACACGGG  
 CATCCATGGCTCCACCTCTCCAGCACACACTCGGGCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCCGAGCTGGCCGCCAGCCCAGCACATACCTGGCGTGGCGAGGAAGTGGCGGATGTT  
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCCGGCCCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGAGGCTTGGGCTGAAAGTGCCGCCTGGTGGCTTAGAGGCTCCCTGTGA  
 GGGAGCAGCCCTCCCCAGA**TAA**ACCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGTCCGCCATGCCCGAGCTCCTGGCACTACCTGAGCCGGAGACCCAG  
 GACTGGCGGCCATGCCCGAGTAGGTTCTAGGGCGGTGCTGGCGCAGTGGACTGGC  
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTCCGTCTGCTTGCTGCCAGCAGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGAAATCTAAACTGGGAATGCCGAGGAGGAAGGGGCTC  
 TGTGCACTTGCAGGCCACGTCAAGGAGAGCCAGCGGTGCCCTGTCGGGGAGGGTTCCAAGGTG  
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGACCT  
 TGTGCATGCATGGCCTCTCTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG  
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG  
 GGTGTTGCTGAGGGCTTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCACTCCC  
 GAGTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGAGCTGCTACAGGACCTGGGA  
 TTGCCTGGACTCCCACCTCCTATCAATTCTCATGGTAGTCAAACACTGCAGACTCTCAAAC  
 TTGCTCATTT

## **FIGURE 66**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLDKLASPKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCOSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVALADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSvreQPLPR
```

**Signal peptide:**

amino acids 1-17

**FIGURE 67**

GAAGTCGCGAGCGCTGGC**ATG**TGGCCTGGGGCGCGCTGGCGCGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGCGACACGTTCTCGGCCTGAC  
 CAGCGTGGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGCTGCTGAGGCAGTACCTGC  
 GCGGGAGGAGGCGCGGCTGCGGACCTGACTAGATTCTACGACAAGGTACTTCTTGAT  
 GAGGATTCAACAACCCCTGTGGCTAACCTCTGCTGCATTTACTCTCATCAAACGCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTGAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTCCAGGCCCTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTTTCTCTCA  
 CAGGGATGACTGCTCCAAGTTGGCAAGGTGGCTATGACATGGGGATTATTACCATGCC  
 ATTCCATGGCTGGAGGAGGCTGTCAGTCTTCCGAGGATCTACGGAGAGTGGAAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTGGATCACTGGCCTTGCTTATTCCGGCAGGAA  
 ATGTTCTGTTGCCCTCAGCCTCTCAGGGAGTTCTCTACAGCCCCAGATAATAAGAGG  
 ATGCCAGGAATGTCTGAAATATGAAAGGCTTGGCAGAGAGCCCCAACACGTGGTAGC  
 TGAGGCTGTCATCCAGAGGCCAATATACCCCACCTGCAGACCAGAGACACCTACGAGGGC  
 TATGTCAGACCCCTGGGTTCCAGCCCACCTCTACAGATCCCTAGCCTCTACTGTTCTAT  
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCACCCGGAAAGGAGGTACCCACCTGGA  
 GCCCTACATTGCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGCAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAATGGTACCCCTCAA  
 CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCGGCCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTACCAAGC  
 AGCCCCCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATGAGCTC  
 GGTGGAAGCTGGAGGCCACAGCCTCATCTATGCCAACCTCAGCGTGCCTGTGGTAGGA  
 ATGCAGCACTGTTGGTGGAACCTGCACAGGAGTGGTAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCCTGTCCTGGTGGAGATAAGTGGGTGGCAACAAAGTGGATACTGAGTATGG  
 ACAGGAATTCCGCAGACCCCTGCAGCTCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAC  
 TGGTGGAGTCCTGTCCTGAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCTGGAAGAAGGCCTGTCAGCTTGTCAGCTGTGCCTCGCAAATCAGAGG  
 AAGGGAGAGGTTGTTACCAAGGGACACTGAGAATGTACATTGATCTGCCAGGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGAGTGGAGGCCTGAGAGGGAAGTTCTGG  
 AGTTCAAGATACTCTGTTGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGTC  
 TTTGGCACTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCCAGAACCTTAAGACTTTCTCCCCACTGCCTCTGCTGCAGCCAAAG  
 CAGGGAGTGTCCCCCTCCCAGAACGATATCCCAGATGAGTGGTACATTATATAAGGATTTT  
 TTTAAGTTGAAACAACTTCTTTCTTTGTATGATGGTTTTAACACAGTCATTA  
 ATGTTATAAATCAAAA

## **FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAI PWLEEAVSLFRGSYGEWKTEDEASLEDALDHЛАFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHQLQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDTLHAGCPVLVGDKWANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19

**FIGURE 69**

GAGATAGGGAGTCTGGTTAACGTTCTGCTCCATCTCAGGAGCCCTGCTCCCACCCCTAG  
 GAAGCCACCAGACTCCACGGTGTGGGCCAACAGGTGGAATCGGCCCTGGCAGGTGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCGTAACCCGCGCGGGAG  
 CGCCCAGG**ATG**CCGCGCGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCT  
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCTTGAAAGTGCCTTCC  
 TGGCTCCAGCCATCATCCTCATCCTCTGGCGTCGTATGTTCATGGTCTCCTTCAATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTATGTACATCCTGGAT  
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGAACCAGACCATTG  
 ACTTCCTGAACGACAACATTGAAAGAGGAATTGAGAACTACTATGATGATCTGGACTTC  
 AACATCATGGACTTTGTTCAAGAAAAGTTCAAGTGCTGTGGCGGGAGGACTACCGAGATTG  
 GAGCAAGAATCAGTACACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGTGCCCTACA  
 CCTGCTGCATCAGGAACACGACAGAACAGTTGTCAACACCATGTGTGGCTACAAACTATCGAC  
 AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGCTGCACCAACGCCGTGATCAT  
 CTGGTTCATGGACAACACTACACCATCATGGCGTGCATCCTCTGGCATTGCTTCCCCAGT  
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGTGGAGGACATCATGGAGCAC  
 TCTGTCACTGATGGCTCCTGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGAGGCACGGG  
 ATGCTGTTGTGCTACCCCAAT**TAG**GGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCGGCCCTCTGCCACA  
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGGCCTCTGCCCTC  
 CCCAGGGAGCAGAGCCTGGCCTCCCTAACAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT  
 GCCCACCTGGGCCTGGGAACAAGGCCCTCTTCTCCAGGCCTGGCTACAGGGAGGGA  
 GAGCCTGAGGCTCTGCTCAGGGCCATTTCATCTGGCAGTGCCTGGCGGTGGTATTCAA  
 GGCAGTTTGTAGCACCTGTAATTGGGAGAGGGAGTGTGCCCTCGGGCAGGAGGGAAGG  
 GCATCTGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCAGGTTGGC  
 CTCTCTCAGCCTCCAGGTGCCTTGAGCCCTTGCAGGGCGGCTGCTTCTTGAGCCTA  
 GTTTTTTACGTGATTTGTAACATTCACTTTGTACAGATAACAGGAGTTCTGAC  
 TAATCAAAGCTGGTATTCCCCGATGTCTTATTCTGCCCTCCCCAACAGTTGTTAA  
 TCAAACAATAAAACATGTTGTTGTTTAAAAAA

## **FIGURE 70**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGIENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPAGAKPSVEAAGTGCCLCYPN
```

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTCCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
 CACCTGGGAAG**ATG**GCCGGCCCGTGGACCTTCACCCTCTGTGGTTGCTGGCAGCCACC  
 TTGATCCAAGCCACCCCTCAGTCCCAC TGCA GTTCTCATCCTCGGCCAAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCATGCCGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTGAACACC  
 GTCCTGAAGCACATCATCTGGCTGAAGGTATCACAGCTAACATCCTCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCCTGGCCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCA ACTGCTGTATAAGCTCCTCCTGGTGAACGCCCTAGCTAAGC  
 AGGTATGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAAACCAGCTGTGTCCCCTG  
 ATCGAGGCTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC  
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTACACCCATT  
 AGCTCTACCTGGGGCCAAGTTGGACTCACAGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTCCCTGACAATGCCACCCCTGGACAACATCCGTTAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATTCAAGGTGCTGGTGG  
 ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGCTGATCAATGAAAG  
 GCTGCAGATAAGCTGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCAAGTGATCGTGTGGAAAGTGGTCCCTCCA  
 GTGAAGCCCTCCGCCCTTGTTCACCCGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC  
 ACCAAAGGTGACCAACTTAACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAACATCATCACTGAGATCATCC  
 ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAAGATCTGGGTCCCAGTGTATTGGTG  
 AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTACTGACCAAGGATGCCCTGTGCTTACTCC  
 AGCCTCCTGTGGAAACCCAGCTCCTGTCTCCAG**TGA**AGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAAT  
 CAATAAACACTGCCTGTGAAAAA

**FIGURE 72**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGIPLGSLVNTVLKHIILWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL
PESAHLRKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSLRQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAAESSLTKDALVLTPASLWKPSSPVSQ

```

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTGGCGTTTGGTGTCTCTGTGACCATGGTGGCGCTG  
 CTCATCGTTGCGACGTTCCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA  
 AAAGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCCGTCGCCTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
 CTCCAAGTGCATAGACAGTGTGCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC  
 AAACCTCCTGGCGATACTCCAGTGCATTCAACACAGGATATTTTGCCATGGTGGATTTG  
 ATGAAGGCTCTGATGTATTCAGATGCTAAACATGAATTCAAGCTCCAACCTTCATCAACTTT  
 CCTGCAAAAGGGAAACCAAACGGGGTGAACATATGAGTTACAGGTGCGGGTTTCAGC  
 TGAGCAGATTGCCCGGTGGATGCCGACAGAACTGATGTCAATATTAGAGTGAATTAGACCCC  
 CAAATTATGCTGGTCCCCTATGTTGGGATTGCTTTGGCTGTTATTGGTGGACTTGTGTAT  
 CTTCGAAGAAGTAATATGGAATTCTCTTTAATAAAAAGTGGATGGGCTTTGCAGCTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACACCATATGCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCACTCAAGCCCAGTTGTA  
 GCTGAAACACACATTGTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGCTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGAAAGCGAAAGATAATGTGTGGCTGGTATTG  
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTATTAGTCAAATATCATGGCTAC  
 CCATACAGCTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAAATCGTGTGTTGAAAAGAAGAATGCAACTTGTATATTGTATTAC  
 CTCTTTTTCAAGTGATTAAATAGTTAACCTAACAAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTGAAAATAATTATCCTCTAACCTCTCTT  
 CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAGTATATTATAAAAATTGTAAAA  
 CTACTACTTGTGTTAGTTAGAACAAAGCTCAAAACTACTTGTAACTGGTCATCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCCACATATGCC  
 TGTACAGATAACTACATTAGGAATTCTAGCTTCTCATCTTGTGGATGTGTAT  
 ACTTTACGCATCTTCTTTGAGTAGAGAAATTATGTGTGTCTGGTCTTCTGAAAATG  
 GAACACCATTCTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTCTCCTCCT  
 GCATATTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTAAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTCTGCTTGAGTATGGTGTAACTACCTGTATTAGAAA  
 GATTTCAGATTCCATTCCATCTCCTTAGTTCTTAAGGTGACCCATCTGTGATAAAAATA  
 TAGCTTAGTGTCAAAATCAGTGTAACTTATACATGGCCTAAATGTTCTACAAATTAGAGT  
 TTGTCACCTATTCCATTGTACCTAAGAGAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTACGCCTGTAATCTCAGCACTTGGGAGGCCAAGGCAGGCAGATCAC  
 GAGGTCAAGGAGTTGAGACCATCTGCCAACATGGTGAACACCCCGTCTCTACTAAAAATAT  
 AAAAATTAGCTGGGTGTGGTGGCAGGGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACCTGAACACTCAGGAGATGGAGGTTCACTGAGGCCAGATCACGCCACTGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTAAAAAA

## **FIGURE 74**

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKVSQMLEWTNKRPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

## **FIGURE 75**

## **FIGURE 76**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPsRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLRQEGRPMVNLIIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSVLDIYPTMLDIAGIPL
PQNLSGYSILLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMN PRAV
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**  
 GCCTCTCTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTGGGCACACT  
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
 TGTGACATCTATAGCACCCCTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCGAGCAAAGACAGACTGGCGGTAGCAGGTGGAGTCTTTTC  
 ATCCTTGGAGGCCTCCTGGGATTCAATTCTGTTGCCCTGGAATCTCATGGGATCCTACGGGA  
 CTTCTACTCACCACCTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGGCTTTACTTGG  
 GCATTATTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCC  
 CAGAGAAATCGCTCCAACACTACGATGCCTACCAAGCCAACCTCTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT  
 ATGTG**TGA**AGAACCAAGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTCAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTTGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTTCTCACCTGCTGCTC  
 CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTGCCTCTGGTTACCTGGACTCCATCCCCAAACCCACTAATCACATCCACTG  
 ACTGACCCCTCTGTGATCAAAGACCCTCTCTGGCTGAGGTTGGCTTAGCTATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTTGTATGACTCCACAGTGTCC  
 AGACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGAAACAGAAAGCAG  
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTAAAAAAATA

## **FIGURE 78**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLLGTILVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSVSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVVAWLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCAC TGCT GCT GTCCC ATCAG CTG CTGA AGCT CC **ATG** GTGCC AGA ATCT CGCT CCT GC  
TTAT GTGT CAGT CTG TCT CCT CCT CTT GTGT CCA AGGG AAGT CAT CGCT CCC GCT GGCT CAG  
AACC ATGG CTGT GCC AGCC GGC ACC CAGGT GTGG AGACA AGAT CTACA ACCC TTGG AGC AG  
TGCT GTT ACA ATGAC GCC ATCG TGT CCT GAG CGAG ACC CGCC AAT GTGG TCCCC CTGC AC  
CTT CTGG CCT GCT TGT GAG CTCT GCT GTCT GATT CCTT GGCT CACAA ACAG ATT TT GTG  
TGA AGCT GAAG GTTC AGGG GTGA ATT CCC AGT GCC ACT CAT CTCC ATCT CCAG TAA AT GT  
GAA AGC AGA AGAC GCT TT CCC **TGA** GAAG ACAT AGAA AGAA ATCA ACT TT CACT AAGG CAT C  
TCAG AA ACAT AGG CTA AGG TAAT AT GTGT ACC AGT AGAGA AGC CTGAGGA ATT TACAA ATG  
ATGC AGCT CCA AGCC ATT GTAT GGCC ATGT GGG AGACT GAT GGG ACAT GGAGA ATGAC AGT  
AGATT ATCAGG AAATAA ATAA AGT GGTTT CCA ATGT ACAC ACCT GTAAAA

## **FIGURE 80**

MVPRIFAPAYVSVC~~LLL~~CPREVIAPAGSEPWL~~C~~Q~~P~~APRCGDKIYNPLEQCCYND~~A~~IVSLSE  
TRQCGPPCTFWPCFELCLDSFGLTNDFVVKLKVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

## **FIGURE 81**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTGCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTCTACGACCCCCTGCAGCACTGTT  
GCTATGATGATGCCCGTGCCTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA  
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAAACCAGAACTGCGA  
CTCAGCCGGACCTCGGATGACAGGCTTGTGGCAGTGTCAGATGGAACATCAGGGAA  
CGATGACTCCTGGATTCTCCTCCTGGGTGGGCCAGAGAAACACACACTCAACTGCCACTTCATT  
TCTGGGATGCTGAGTGGCTGTTGGGCCAGAGAAACACACACTCAACTGCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCAACCCAAAGGCTGGCTGGGAACCCTTCACCC  
TCTGTGAGATTTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTATGTACTTATAAATGAAAA

## **FIGURE 82**

MAPRGCIVAVFAIFCISRLLCSHGAPVAPMTPYLMCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTRVCFEQCCPWTFMVKLINQNCDARTSDDRLCRSVS

### Signal peptide:

amino acids 1-24

## FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGCAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCCGGCGTCCGCCGCTCCCCGGCACCAAGATTCCTCT  
 GCGCGTCCGACGGCGAC **ATGGCGT**CCCCACGCCCTGGAGGCCAGCTGGCGCTGGGA  
 TCCCTGCTCTCGCTCTTCCCTGGCTCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTCGC  
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGCAGAACGTACCCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GGCGAGGTGCAGACCTGCTCAGAGGCCGGCCATCGAACCTCACGTTCCAGGACCTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTAGGCCACGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGAACCTGACCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACGTGTGGTGT  
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACCGCCGTGCCAGGAGCTGGTGCAGACAGAACATTCAAGGGATTGAAAACC  
 CCGGCTTGAAAGCCTCACCACCTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG  
 TCCTATGTGCCAGCGGCAGCCTCTGAGTCTGGCGGCATCTGCTTCGGAGCCCAGCAC  
 CCCCTGTCTCCTCCAGGCCCGAGACGTCTTCCATCCCTGGACCCGTCCCTGACT  
 CTCCAAACTTGAGGTATC **TAG**CCCAGCTGGGGACAGTGGCTGTTGGCTGGGTCTGG  
 GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTGGCTCGGCCCTGGTTC  
 CCTCCCTCTGCTCTGGCTCAGATACTGTGACATCCCAGAACGCCAGCCCTCAACCCCTC  
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCCTGTCCAAGGATTTGGGTGCTGAG  
 ATTCTCCCCTAGAGACCTGAAATTACCAAGCTACAGATGCCAAATGACTTACATCTTAAAGAA  
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTGTTCTGAGACATGAGCCTGGATGTGGCA  
 GCATCAGTGGACAAGATGGACACTGGCCACCCCTCCAGGCACCAAGACACAGGGCACGGTG  
 GAGAGACTTCTCCCCGTGGCGCCTGGCTCCCCGGTTTGCCCGAGGCTGCTCTCTGTC  
 AGACTTCTCTTGTAACACAGTGGCTCTGGGCCAGGCCTGCCACTGCCATGCC  
 ACCTCCCCAGCTGCCCTTACCAAGCAGTTCTGAAGATCTGTCACAGGTTAAGTCAAT  
 CTGGGGCTTCACTGCCATGCCATTCCAGTCCCCAGAGCTGGTGGTCCGAAACGGGAAGTAC  
 ATATTGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCAACCACTGGAGATGGTGTGAGGGAGGTGGTGGGCCCTCTGGAAAGGTGA  
 GTGGAGAGGGCACCTGCCCTCCCCATCCCTACTCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCACACAATGTCTGTCCACCCCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAAGA

## **FIGURE 84**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASILGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSEERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLEASAD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSQ
DSENITAAALATGACIVGILCLPLLLLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPPGDVFVPSLDPVPDSPNFEVI
```

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

## FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCT  
 TTCCCCGCGTTCTCTTCCACCTTCTCTTCTTCCCACCTTAGACCTCCCTCCTGCCCTCC  
 TTTCCTGCCACCAGCTGCTTCCCTGGCCCTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTCGTCTCCCTCCTCCCAGA  
 CTCCGCTCCGGACCAGCGGCCTGACCCGGAAAGG**ATG** GTTCCCGAGGTGAGGGTCCTC  
 TCCTCCTTGCTGGACTCGCGCTGCTCTGGTCCCCCTGGACTCCCACGCTCGAGCCCGCCC  
 AGACATGTTCTGCCTTTCCATGGAAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACT  
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGGCCATGTGAGT  
 TGTACCGCCTCCACTGTCCGCTGTCACTGCCCGGACCCCTGTGACGGAGGCCACAGCAATG  
 CTGTCCTAACGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCACCAAAGTCCTGCC  
 AGCACAAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCCATGAGCTGTTCCCCCTCC  
 CGCCTGCCAACCAACCAGTGTGTCCCTGCAGCTGCACAGAGGGCCAGATCTACTGCCGCTCAC  
 AACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAACGCT  
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGGGCCGGCACCCAGC  
 CCCCACGGCCTCAGCGCCCCCTGAGCTTCCATCCCTGCCACTTCAGACCCAAGGGAGCAG  
 GCAGCACAACTGTCAAGATCGCCTGAAGGAGAAACATAAGAAAGCCTGTGCATGGCGGG  
 AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTCCGTGCCTTCGGCCCCCTGCCCTG  
 CATCCTATGCACCTGTGAGGATGGCGCCAGGACTGCCAGCGTGTGACCTGTCACCGAGT  
 ACCCGTGCCTCACCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGACAAA  
 GCAGACCCGGCCACAGTGAGATCAGTCTACCAAGGTGTCCTGAAGGCACCGGGCCGGTCCT  
 CGTCCACACATCGGTATCCCCAAGCCCAGACAAACCTGCGTCGCTTGCCTGGAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTCCACTTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCCAC  
 GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCGGAGCTGAAGGTACGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAAGACC**TAA** CAGTTGCAGATATGAGCTGTATAATTGTTGTT  
 ATTATATATTAATAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAA

## FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCCSSDAGRKRGPGBTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLSDSDQESQEARNPERGTALPTARWPPRRSLERLPSDPG
AEGHGQSRQSDQDITKT
```

**Signal peptide:**

amino acids 1-25

## FIGURE 87

## FIGURE 88

MDSLRKMLISVAMLGAGAGVGYALLVITPGERRKQEMLKEMPLQDPRSREEAARTQQLLA  
TLQEAATTQENVAWRKNWMVGGEGGASGRSP

**Signal peptide:**

amino acids 1-18

## FIGURE 89

## **FIGURE 90**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLIFLLSGPLQGQQHHLVEYMERLAALERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAEAAFVICGTLVVVYNTRPASRARIQCSFDASGTLTPERAALPYFPERRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTAGAACAGCGCAGTTGCCCTCCGCTACGCAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCAATCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG  
 CTCTCATGCTCAGTTGGTTCTGAGTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTCCGTGTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTCAGGGCCAGTTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAAACTGGTGAAGGATTCTATTGGGTGCAGGATTAGTCCCAGTCTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTCAGCACTGGCTCAGTTCTCATTCCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTCACTCCTCAGGGCTGGTCCCCGGCCACAGCGAAGTG  
 GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
 TGTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTCGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAAATACTCTGCTGTGGCTATTTTG  
 GCATTGTTGACTGAAGATTCTTCTCCAAATTCCAGTGGAAAATCCAGGGGAACTGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTCACCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGGCT  
 TCTCAGAGTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAGGTG  
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGGAGGTACGTGACTTGTCTCCG  
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTGTATTACATTAATCCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGTCTCCTGGACTATGAGTG  
 TGGGACCATCTCCTCTTCAACATAATGACCAGTCCCTTATTACCCCTGACATGCGGT  
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAATGGAACTCCC  
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCTTGGCAAAGGGCTCTGC  
 AATCCCAGAGACAAGAACAGTGAATGAGTCCTCACAGGCAACCACGCCCTCCAGGG  
 GTGAAATGTAGGATGAATCACATCCCACATTCTCTTAGGGATATTAAGGTCTCTCCCA  
 GATCCAAAGTCCCGCAGCAGCCGGCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC  
 ACATGGGAGTCAGGTGTCACTGGCTGCCCTGAGCTGGGAGGGAAAGAAGGCTGACATTACATT  
 AGTTGCTCTCACTCCATCTGGCTAAGTGATCTGAAATACCACCTCAGGTGAAGAACCG  
 TCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCAATTACACTTTCAGTA  
 AAAAAA

**FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPDKPQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMOMPQYQGRTKLVKDSIAEGRISLRLLENITVLDAGLYGCRISQSYYQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPGQDLSTDRTNRDMH  
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAEQELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL  
PDHGYWVRLNGEHLYFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## FIGURE 93

GCGATGGTGCGCCGGTGGCGGTGGCGCGCGGTGCAGGCTTCCTGGTCGGATTGCA  
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGGCGGAGCCGAGCGC  
CATGAGGAGCCTGCCGAGCCTGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCC  
 CGCTCGCCTCAGCCGCCTCGGCGGGAATGTCACCGGTGGCGGGGCCGCCGGCAGGTG  
 GACCGCGTCGCCGGGGCCCGGGTTGCGGGGCAGCCCAGCCACCCCTCCCTAGGGCGACGCC  
 TCCCACGGCCCAGGGCCCCGAGGACCGGGCCCCCGCGCCACCGTCCACCAGACCCCTGGCTG  
 CGACTTCTCCAGCCCAGTCCCCGGAGACCAACCCCTTTGGGCGACTGCTGGACCCCTTCC  
 ACCACCTTCAGGCGCCGCTGGCCCTCGCCGACCACCCCTCCGGCGGCGAACGCACCTC  
 GACCACCTCTCAGGGCGCCGACCAGACCCCGCGCCGACCACCCCTTCGACGACCACGGGCCGG  
 CGCCGACCACCCCTGTAGCGACCAACCGTACCGCGCCACGACTCCCCGGACCCGACCCCG  
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCCACCCCTGCCACCGAGGCCCCCTC  
 TTCGCCTCCTCCAGAGTATGTAACTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACACAGGGCAGTGTGAGTGTGGCCAGGTATCAGGGGCTCTGTCAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATAACCGTGCAACAGGTAAGAACAGAGGGTGGAACTGAAGTTTATT  
 TTATTTAGCAAGGGAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTAAACAAAG  
 GAGGATGAGGGTCAAGATTACAAAATATTTATATACCTTTATTCTCTTACTTTATATGT  
 TATATTAAATGTCAGGATTTAAACATCTAATTACTGATTTAGTTCTTC  
AAAGCACTAGAGTCGCAATTTCAGGATAATTCTGTAAATTCTCATGGGAAAAAAATTATTGAAGAAT  
 AAATCTGCTTCTGGAAAGGGCTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTTCTT  
 ATGTTATTAAATATACATTGGAGTTGAGGAATTGTTGTTGGTTATTTCTCTCTA  
 ATCAAAATTCTACATTGTTCTTGACATCTAAAGCTTAACCTGGGGTACCCCTAATT  
 TTTAACTAGTGGTAAGTAGACTGGTTACTCTATTACAGTACATTGAGACCAAAAG  
 TAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAATTAAATCTAGTGGA  
 ATAATGTAAGTGTATCTAAGCATTGCGCTTGACTGCACTGAAAGTAATTATTCTTGACCT  
 TATGTGAGGCACCTGGCTTTGTGGACCCCAAGTCAAAAAACTGAAGAGACAGTATTAAAT  
 AATGAAAAAAATAATGACAGGTTACTCAGTGTAACTGGTATAACCCAAAGATCTGCTGC  
 CACTTACGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTGTTCTCTCAAG  
 GTTGTGTTGAGATTAAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGGTTGTTAATTCAAAGGAATTATGGACTGAAATGAGAGAACATGTTAAGA  
 ACTTTAGCTCCTTGACAAAGAAGTGTAACTTTAGCACTAAATATTAAATGCTTTA  
 TAAATGATATTATACTGTTATGGAATTATGTATCATATTGTAGTTATTAAAAATGTAGAAG  
 AGGCTGGCGCGGTGGCTACGCCTGTAATCCTAGCACTTGGGAGGCCAGGCAGGTGGAT  
 CACTTGAGGCCAGGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACACCCGTCTACTAAA  
 AATACAAACAAATTAGCTGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT  
 GAGGCAGGAGAACCGGTTGAACCCGGGAGGTGGAGGTTGAGCTGAGATCGCGCCACT  
 GCACTCCAGCCTGGTGGAGAGAGGGAGACTCTGTCTAAAAAAAAAAAAAA

## **FIGURE 94**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSILPSLGGLALLCCAAAAAVASAASAGNVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTLSTTGAPTTPVATTVPAPTPRTPTPDLPSSNSSVLPTPPATEAPS
SPPPEYVCNCNSVVGSLNVNRCNQTTGQCECRPGYQGLH CETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTCTGGCTTGG  
TCTCGGTGCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTTCTGG  
CCCTGGTACGTGCTTGGCTCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGTGGTGGTGGCAGAAAACAACCTGCGGACGCTGTCCCTCTC  
AGCACGGCTGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCACCAACTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTCGGGGACGAGCCCTAACACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGGCCAGGAGGCCATGGGCTTCAACAGTGGAGCAGGAGC  
CTGGGCTTCTGTACAG**TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTACAAGAT  
CCTTCTGTGAGTGCTCGTCCCCAGTAGGGATGGCGCCACAGGGCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGCCAGCACCAAGCTCAGAATAAAGCGATT  
CACAGCA

## **FIGURE 96**

MGGLLLAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRSLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

## FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGCAGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGCAGGAAGGCCGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
 GGCTGGATTTACCTGGCCCAGTAGTCATGGCTACTGGTCCGGGAAGGGGCCAATACAGA  
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCCACCTCCTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATTGAGAGATGCCAGA  
 AGAAGTGATGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCAG  
 GCACCCCTGGAGTCCGGCTGCCCTCAGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG  
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
 CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCCTAC  
 CCGCCTCAGAACTTGACCATGACTGTCTCCAAGGAGACGGCACAGTATCCACAGTCTGGG  
 AAATGGCTCATCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCCTGTGCC  
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTGGTGCACCTGAGGGATGCAGCTGA  
 ATTACACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCC  
 AGAGCAAAGCCACATCAGGAGTGAUTCAGGGGGTGGTGGGGAGCTGGAGGCCACAGCC  
 GTCTTCCTGTCCTCTCGTCATCTCGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGGAGATAACGGCATAGAGGATGCAAACGCTGTCAGGGTTCAGCCT  
 CTCAGGGGCCCTGACTGAACCTGGCAGAACAGACTCCCCAGACCAGCCTCCCCAGCT  
 TCTGCCCGCTCCTCAGTGGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
 GAAGCCTTGGGACTCGCGGGACAGGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
 ACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTAAACCTGAAT  
 CCACACTGTGCCCTCCCTTATTTTTAACTAAAAGACAGACAAATTCTA

## **FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHPCSFYPSHGWIYPGPVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRSDAGRYFFRMEKG  
SIKWNYKHHRLSVNVNTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS  
PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMVFQGDG  
TVSTVLNGNSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLNVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
CRKKSARPAAGVGDTGIEDANAVRGASQGPLTEPWAEDSPPDQPPPASARSSVGEHELQYA  
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## FIGURE 99

GACGCCAGTGACCTGCCGAGGTGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTCACCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTCCGGAGGACAGGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGCGGTGGAAAGTTGGAAGGCCACGTTCACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT  
ACATCTTTACTGCAAAGACCAGCACCATGGGGCCTGCTCCACATGGAAAGCTTGTGGGT  
AGGAATTCTGATAACCAACCGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTCACGCCCTGCAGACGGGAAGCTGCCTCCGAACACTAGG  
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCCTACCACCAAGACACAGAGCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCCTCCCTGCTCCCACCCACCTGACTCCAAATAAGTCCT  
TTTCCCCCAAA

## **FIGURE 100**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

**Important features:**

**Signal peptide:**

amino acids 1-17

**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTCGGGACTGGAAGTCATCGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATGCCCGGAGATGGCTCCTGACAGCAGCCCAGTGCCTCAAGCCCCGCTACA  
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTCCCCACCCGGCTTCAACAAACAGCCTCCAAACAAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCAGTGCCTGGCACAGCTGCCTCATTCGGCTGGGCAGCACGTCC  
AGCCCCCAGTTACGCCTGCCTCACACCTTGCATGCGCAACATCACCATCATTGAGCACCA  
GAAGTGTGAGAACGCCTACCCCGAACATCACAGACACCATGGTGTGTCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGAETCCGGGGCCCTCTGGTCTGTAACCAGTCTCTT  
CAAGGCATTATCTCCTGGGCCAGGATCCGTGCGATCACCCGAAAGCCTGGTGTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATAGACTGGACCCA  
CCCACCACAGCCCATCACCCCTCATTCCACTGGTGTGTTGGTCTGTTCACTCTGTTAAT  
AAGAAACCTAAGCCAAGACCCCTACGAACATTCTGGCCTCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTTGATCCCCAGCCCCA  
AAGACAGCTCCTGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 102**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTA
HCLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHNDIMLVKMASPVSIT
WAVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIEHQKCENAYPGNITDT
MVCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN
```

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTCTGCTGGAGCCGATGCCAAAACCATGCATTCTTATTCA  
GAGATTCATTGTGGGCCTTTACTGCTCAGAGACAAAAGAAAGAGGAGACCGAAGAA  
GTGAAAATAGAAGTGGCATCGTCAGAAAAGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGA  
CACAAAATGAAGGCCACCCAAATGGTTGTTGGCTGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATA  
ACCCCTTCATTGTCATAACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATT  
AGATTGAACCTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGAAATTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTAGAAGATATTTAAGA  
AGAATGACCATGATGGTATGGCTTCATTCTCCAAGGAATACAATGTATA  
ACCAACACGATGAACTAGCATATTTGTATTCCTACTTTTTAGCTATTACTGTACTTTATGTATA  
AAACAAAGTCACTTCTCCAAGTTGATTTGCTATTTCCCCTATGAGAAGATATTTGA  
TCTCCCCAATACATTGATTTGGTATAATAATGTGAGGCTGTTGCAAAC  
TTAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAA

## **FIGURE 104**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVI PPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIEFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDGFISPKEYNVYQHDEL
```

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

**FIGURE 105**

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTGGAGCT  
GTGACTCAGAAAACCAAAACTCCTGTGCTAAGTGCCCCCAAATGCTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTCTGGATCTGGCAGAAACTATTCACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCCTG**TAA**TCCCAGTTCTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTAGGAGTTGAGACCAGCCTGGCAACATAGTGAACAC  
CCCGTGTCTACTAAAAATACAAAATCAGCCGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAGAAAAGA  
TAGTTTCTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

## **FIGURE 106**

MQGPLLLPGLCFLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL  
ETCNARHGGSL

### Signal peptide:

amino acids 1-18

## **FIGURE 107**

CAAGCAGGTCACTCCCTGGTGACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC  
AGGGAAAGGGTACCTCTGAGATTCCCTTCCCCAGACTTGGAAAGTGAACCACCA**ATGG**  
GGCTCAGCATTTTGTCTGTGTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC  
CAGCCTGCGCTGCGGGGTGTCCTATTGACCACAGGTGGGCTCACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGAACACAGCCTCAGCCAGCTGACTGGACCGAG  
CAGATCCGGCACAGCGGTTCTGTGACCCATCCGGTACCTGGAGCCTGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCGCCTGCCGTCCCGTAACCAGCAGCGTTCAAC  
CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGC  
ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCTAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTATCCGGAGAACATCAGGAGAACATGGTGTGCAAG  
GCGCGTCCGGGCAGGATGCCAGGGTATTCTGGGGCCCTGGTGTGGGGGA  
GTCCTCAAGGTCTGGTGCCTGGGGTCTGTGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACA**TGA**  
CTGTTCCACCTCCACCCACCCCTTAACCTGGTACCCCTCTGCCCTCAGAGCACC  
AATATCTCCTCCATCACTCCCTAGCTCCACTCTGTTGCCCTGGAACTTCTGGAACTT  
TAACTCCTGCCAGCCCTTAAGACCCACGAGCAGGGTGAGAGAAGTGTGCAATAGTCTGG  
ATAAAATATAATGAAGGGAGGGCAAAAAAAAAAAAAAA

**FIGURE 108**

MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDGGPLVCGGVLQGLVSWGSVGPQDGIPGVYTYICKYVDWIRMIIMRNN

**Signal peptide:**

amino acids 1-17

W: Valine  
R: Lysine  
K: Arginine  
E: Glutamic acid  
D: Aspartic acid  
S: Threonine  
T: Serine  
C: Cysteine  
Y: Tyrosine  
F: Phenylalanine  
I: Isoleucine  
V: Alanine  
M: Methionine  
H: Histidine  
P: Proline  
A: Alanine  
G: Glycine  
N: Asparagine  
Q: Glutamine  
L: Leucine  
D: Aspartic acid  
E: Glutamic acid  
S: Threonine  
T: Serine  
C: Cysteine  
Y: Tyrosine  
F: Phenylalanine  
I: Isoleucine  
V: Alanine  
M: Methionine  
H: Histidine  
P: Proline  
A: Alanine  
G: Glycine  
N: Asparagine  
Q: Glutamine  
L: Leucine

## FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCTGTGCCTCCTCGTCCCTCGC  
 CGCGTCCGCGAAGCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGCGAGCTCAGCA  
 ACAGGTTCCAAGGAGGGAAAGCGTTGGCTTGCTCAAAGCCGGCAGGAGAGGAGGCTGGCC  
 GAGATCAACCAGGGAGTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCAGAAAA  
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTGACCTGAACAATGAAGGCAGATTGACC  
 TGATGTCTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
 AAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATATCCTACCGAGACTTGTGAA  
 CATGATGCTGGGAAACGGTCGGCTGCCTCAAAGTTAGTCATGATGTTGAAGGAAAAGCCA  
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCC**TGA**  
 GGACCCCGCCTGGACTCCCCAGCCTCCCACCCATACCTCCCTCCGATTTGCTGCCCTT  
 CTTGACACACTGTGATCTCTCTCTCATTGTTGGCATTGAGGGTTGTTGTGTT  
 TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTAAAGGGCTCTGGTCGGGAATCC  
 TGAGCCTGGTCCCCCTCCCTCTCTTCTCCCTCCCCGCTCCGTGCAGAAGGGCTG  
 ATATCAAACCAAAACTAGAGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
 CTCACTTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTCAGGCTC  
 ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
 CTGCAGGGCCTTTGGGTTCTGGACAGTGCCTGGTCCAGTGCTCTGGTGTACCC  
 AGGACACAGCCACTGGGGCCCCGCTGCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
 CATCCTCAGTGATGTGAAGGTGGAAAGGAAAGGAGCTTGGCATTGGAGGCCCTCAAGAAGG  
 TACCAAGGAACCCCTCAGTCCTGCTCTGGCACACCTGTGCAGGCAGCTGAGAGGCAG  
 CGTGCAGCCCTACTGTCCCTACTGGGGCAGCAGAGGGCTCGGAGGCAGAAGTGAGGCCTG  
 GGGTTGGGGAAAGGTCACTGCTGTTCCACCTTGTAGGGAGGATACTGAGGGAC  
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
 CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTGAAAAA

## **FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVM  
MFEGKANESSPKPVGPPPEDIASLP

### **FIGURE 111A**

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTGCCCGCAGAGGCAGGCCCTCCCG  
GGAGCGGGGCCCTGCACACC **ATG** GCCCCCGGGTGGCAGGGTGGCGCCGCCGCG  
CGCCTGGCGCTGGCCTGGCGTGGCGAGCGTCTGAGTGGGCCTCCAGCGTCGCCTGCC  
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGGCCTCCCGCGGGTC  
CTCGGGCATCCCCGCAACGCTGAGCGCCTGACCTGGACAGAAATAATATCACCAAGGATC  
ACCAAGATGGACTTCGCTGGCTCAAGAACCTCCGAGTCTTGCATCTGGAAAGACAAACCAGGT  
CAGCGTCATCGAGAGAGGGCCTTCCAGGACCTGAAGCAGCTAGAGCAGTGGCAGTGCCTGAACA  
AGAATAAGCTGCAAGTCCTCCAGAATTGCTTTCCAGAGCACGCCAGCTCACCAAGACTA  
GATTTGAGTGAAAACCAGATCCAGGGATCCCGAGGAAGGCCTCCGGCATACCGATGT  
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTCCGAGGC  
TGCAGATTGGAGATCCTTACCCCAACAAACAACATCAGTCGATCCTGGTACCCAGC  
TTCAACCACATGCCAGAGATCCGAACCTGCGCCTCCACTCCAACCACCTACTGCGACTG  
CCACCTGGCCTGGCTCTGGATTGGCTGCGACAGCGACGGACAGTTGCCAGTCACACTCT  
GCATGGCTCCTGTGCATTGAGGGGCTTCAACGTGGCGATGTGCAGAAGAAGGAGTACGTG  
TGCAGCCCCCACTGGAGCCCCATCTGCAATGCCAATCCATCTCCTGCCCTTCGCC  
CTGCACGTGCAGCAATAACATCGTGGACTGTCGAGGAAGGGCTTGATGGAGATTCCGCCA  
ACTTGGCGAGGGCATCGTCAAATACGCCCTAGAACAGAACCTCATCAAAGCCATCCGCCA  
GGAGCCTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAACATCAGATATCGGA  
TATTGCTCCAGATGCCCTCCAGGGCTGAAATCACTCACATCGTGGCTGTGAGTGGAAACA  
AGATCACCGAGATTGCCAAGGGACTGTTGATGGCTGGTCCCTACAGCTGCTCCCTC  
AATGCCAACAGATCAACTGCCCTGGGTGAACACGTTCAAGGACCTGCAGAACCTCAACTT  
GCTCCCTGTATGACAACAAGCTGCAGACATCAGCAAGGGCTTCGCCCTCTGCACT  
CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGTCGACTGCCACTTGAAGTGGCTG  
GCCACTACCTCCAGGACAACCCATCGAGACAAGGGGCCGCTGCAGCACCCGCG  
ACTGCCAACAGCGATCAGCCAGATCAAGAGCAAGAAGTCCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTCAAGCAGCGAGTGCTCATGGACCTCGTGTGCCCGAGAACGTC  
TGTGAGGGCAGGATTGGACTGCTCAACCAGAACGCTGGTCCGATCCAAAGCCACCTCC  
TGAATATGTCACCGACCTGCACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCAACCTGCGAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGAACCAGCT  
GGAGACCGTGACGGCGCGTGTCCGTGCCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA  
GTAACCTGATCAGCTGTGTGAGTAATGACACCTTGGCCGCTGAGTCGGTGAGACTGCTG  
TCCCTCTATGACAATCGGATCACCACATCACCCCTGGGCCCTCACACGCTTGTCTCCCT  
GTCCACCATAAACCTCCTGCAACCCCTCAACTGCAACTGCCACCTGGCTGGCTCGCA  
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGAAACCTAGGTGCCAGAACCCATTTC  
AAGGAGATTCCCATCCAGGATGTGGCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCGCGCTGCCGGAGCAGTCACCTGTATGGAGACAGTGGTGC  
GCAGCAACAAGGGCTCCCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC  
CTGGAGGAACCACCTAACAGCCGTGCCAGAGAGCTGTCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTCAGTAACATGTCTC  
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCCTCAAC  
GGGCTCGGGCCCTGCGAGTGCTAACCCCTCATGGCAATGACATTCCAGCGTCTGAAGG  
CTCCTCAACGACCTCACATCTTCCCATCTGGCGTGGGAACCAACCCACTCCACTGTG  
ACTGCAGTCTCGGTGGCTGCGAGTGGTGAAGGCAGGGTACAAGGAGGCCTGGCATGCC  
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTACCACCCAAACCCACCGCTT  
CCAGTGCAAAGGGCAGTGGACATCAACATTGTGGCAAATGCAATGCCCTGCTGCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCCTGCC

## **FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTACAGCCACAAGGATGGGTCAGCTGCTCCTGCCCTC  
 TGGGCTTGAGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
 AACAAATGCCACCTGCGTGGACGGGATCAACAACACTACGTGTATCTGTCCGCCTAACTACAC  
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGCTGAGCTGAACCTCTGTCAAGCATG  
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTCAAGCTGCGAGGTGTCAGCTGGCTACAGCGGG  
 AAGCTCTGTGAGACAGACAATGATGACTGTGTCAGCTGAGCTGCGACCTGTGTCAGCTGG  
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCTCAGGCTCAGTGGACCCCTGTG  
 AACACCCCCCACCCTGGCTACTGCAAGACCAGGCCATGCGACCAAGTACGAGTGCCAGAAC  
 GGGGCCAGTGCATCGTGGTCAGCAGGAGGCCACCTGCCGCTGCCACCAGGCTGCCGG  
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGCAAAGACTCCTACGTGGAACGTGG  
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGCCACTGACAAGGACAAC  
 GGCATCCTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCAAGGCCACGT  
 GCGGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTACAGTGTGGAGCTGGTACGCTAAACCAGACCCCTGAACCTAGTAGTG  
 GACAAAGGAACCTCAAAGAGCCTGGGAAGCTCCAGAAGCAGCCAGCAGTGGCATCAACAG  
 CCCCCTCTACCTGGAGGCATCCCCACCTCCACCGGCCCTCCGCCAGGGCACGG  
 ACCGGCCTCTAGGCGCTCCACGGATGCATCCATGAGGTGCGCATCAACAAACGAGCTGCG  
 GACTTCAGGCCCTCCCACACAGTCCCTGGGGTGTCACCAGGCTGCAAGTCCTGCACCGT  
 GTGCAAGGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
 GCTGGACCGGCCACTCTGCGACCAAGGGAGCCCTACTGCCGTGCCAGCCGGCTTAGCGGC  
 CATGGAAAATGTGTGGCAACTGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
 GGACTTGTGTGACAACAAGAAATGACTCTGCCATGCCCTCAGCCTCAAGTGTCAACCATG  
 GGCAGTGCCACATCTCAGACCAAGGGAGCCCTACTGCCGTGCCAGCCGGCTTAGCGGC  
 GAGCACTGCCAACAAAGAGAATCCGTGCCCTGGACAAGTAGTCCGAGAGGTGATCCGCCGCC  
 GAAAGGTTATGCATCATGTGCCACAGCCTCAAGGTGCCCATCATGGAATGTCGTGGGGCT  
 GTGGGCCCTAGTGTGCCAGCCCACCCGAGCAAGCGCGGAAATACGTCTCCAGTGCACG  
 GACGGCTCCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCCTGCCCTCGCGTGTTC  
 C**TA**AGCCCCCTGCCGCCCTGCCACCTCTGGACTCCAGCTTGATGGAGTTGGACAGCC  
 ATGTGGGACCCCTGGTACAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA  
 AGAGAAATTAAGTATATTGTAAAATAACAAAAAATAGAACTTAAAAA  
 AAAAAA

## FIGURE 112

MAPGWAGVGA AVR LAL ALA SVLS GPP AVAC PT KCTCSA ASV DCH GL GL RAV PRG I PRN  
 AER LD LDR NNITR IT KMD FAG LKNL RVL HLED NQV S VIER GAF QDL KQL ER LRL NKN K LQVL  
 PELL FQST PKL TR LD LSEN QI QG I PRKA FRG IT DVKNL QLD NNH I S CIED GA FR AL RD LEIL  
 TLNN NN NIS RIL VTS FNH MPKIR T LRL HS N HLY CD CHL AWL SD WLR QR RT V GQFT LCM APV HL  
 RGF NVAD V QK KEY VCP A P HSE P PSC N A N S I C P S P C T C S N N I V D C R G K G L M E I P A N L P E G I V  
 E I R L E Q N S I K A I P A G A F T Q Y K K L K R I D I S K N Q I S D I A P D A F Q G L K S L T S L V L Y G N K I T E I A K  
 GL F D G L V S L Q L L L N A N K I N C L R V N T F Q D L Q N L N L L S L Y D N K L Q T I S K G L F A P L Q S I Q T L H L  
 A Q N P F V C D C H L K W L A D Y L Q D N P I E T S G A R C S S P R R L A N K R I S Q I K S K K F R C S G S E D Y R S R F S  
 S E C F M D L V C P E K C R C E G T I V D C S N Q K L V R I P S H L P E Y V T D L R L N D N E V S V L E A T G I F K K L P N  
 L R K I N L S N N K I K E V R E G A F D G A A S V Q E L M L T G N Q L E T V H G R V F R G L S G L K T L M L R S N L I S C V  
 S N D T F A G L S S V R L L S L Y D N R I T T I T P G A F T T L V S L S T I N L L S N P F N C N C H L A W L G K W L R K R R  
 I V S G N P R C Q K P F F L K E I P I Q D V A I Q D F T C D G N E E S S C Q L S P R C P E Q C T C M E T V V R C S N K G L R  
 A L P R G M P K D V T E L Y L E G N H L T A V P R E L S A L R H L T L I D L S N N S I S M L T N Y T F S N M S H L S T L I L  
 S Y N R L R C I P V H A F N G L R S L R V L T L H G N D I S S V P E G S F N D L T S L S H L A L G T N P L H C D C S L R W L  
 S E W V K A G Y K E P G I A R C S S P E P M A D R I L L T T P H R F Q C K G P V D I N I V A K C N A C L S S P C K N N G T  
 C T Q D P V E L Y R C A C P Y S K G K D C T V P I N T C I Q N P C Q H G G T C H L S D S H K D G F S C S C P I L G F E G Q R  
 C E I N P D D C E D N D C E N N A T C V D G I N N Y V C I C P P N Y T G E L C D E V I D H C V P E L N L C Q H E A K C I P L  
 D K G F S C E C V P G Y S G K L C E T D N D D C V A H K C R H G A Q C V D T I N G Y T C T C P Q G F S G P F C E H P P P M V  
 L L Q T S P C D Q Y E C Q N G A Q C I V V Q Q E P T C R C P P G F A G P R C E K L I T V N F V G K D S Y V E L A S A K V R P  
 Q A N I S L Q V A T D K D N G I L L Y K G D N D P L A L E L Y Q G H V R L V Y D S L S S P T T V Y S V E T V N D G Q F H S  
 V E L V T L N Q T L N L V V D K G T P K S L G K L Q K Q P A V G I N S P L Y L G G I P T S T G L S A L R Q G T D R P L G G F  
 H G C I H E V R I N N E L Q D F K A L P P Q S L G V S P G C K S C T V C K H G L C R S V E K D S V V C E C R P G W T G P L C  
 D Q E A R D P C L G H R C H H G K C V A T G T S Y M C K C A E G Y G G D L C D N K N D S A N A C S A F K C H H G Q C H I S D  
 Q G E P Y C L C Q P G F S G E H C Q Q E N P C L G Q V V R E V I R R Q K G Y A S C A T A S K V P I M E C R G G C G P Q C C Q  
 P T R S K R R K Y V F Q C T D G S S F V E E V E R H L E C G C L A C S

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCTGAGCTGCCTGTACCGACTAGGTGGAGCAGTGTTCCTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGCAGGCACCAGGAATCTGCCTTCAGTTCTGTCT  
CCGGCAGGCTTGAGGAATGAAGGCTGCGGGCATTCTGACCCCTATTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACGGCAAAATATTCTCGAGGGCTGGCTG  
GACAATTACTGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGCCTGGATGACGGCAGCAGTCACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGGAAAGCTGAAGGAGAACACCAGTGCATGTGCCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGAAAAAAGGCTGTGAGGTTCCTAAACTGGAACTGGACCCAGGATGCTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCAAATGCCTGTGTATCTTGTCCCCTTCCCTCCAATA  
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAAGCTATACTTTAAGAAAATAATTTCCAT  
TTAAATGTC

## **FIGURE 114**

MKAAGILTLLIGCLVTGAESKIIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGFQINSFAWCRRGKLKENNHCCHVACSLITDDLTDAIICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

## FIGURE 115

CAGGCCATTGCATCCACTGTCCTGTGTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
 CATGTGTTAAAACGCCAAGCTGAATATATC**ATG**CCCCATTAAAACCTGTACATGGCTCCC  
 CATTGGTTTGAGAAAAGTTCAAGCTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTTCCCAGATCTGCTCTCAC  
 CAAGAGAGATTCTTCTAAACGACTATACAGGGCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTTTAAGGAA  
 ACATTCAAGTCCCTGTCTCACATAGACCCCTGATGTCCTCTATCCATCTAAATGTCACCAG  
 CTTGACTCAGTTGTCCTGAAAAGCTGGATGACCTAGTCCCAAGGGAAAAAATTCTGC  
 TGCTCTCCATCAACAGATAAGGAAAGAAAAATCTGACTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAAGATTGACATCCCAAGATTGGGAGAGGGTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCAGACAAACAGAAAATCTCC  
 CTCCTCCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCACTTGGCATTGTCCC  
 TCTGGAAAGCCATGTACATGCAGTCCCAGTCATTGCTTAATTGGGTGGACCCCTGGAGT  
 CCATTGACCACAGTGTACAGGGTTCTGTGAGCCTGACCCGGTGCACCTCTCAGAAGCA  
 ATAGAAAAGTTCATCCGTGAAACCTCCTAAAGCCACCATGGCCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAATTTCCCTGAAGCATTACAGAACAGCTACCGATATGTTACCAAAC  
 TGCTGGTA**TAA**TCAGATTGTTTAAGATCTCCATTAATGTCATTGATGGATTGTAGACC  
 CAGTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTAAAAAATAAA  
 CTTGAGTCTGAATGTGAGCCACTTCCTATATACCACACCTCCGTCCACTTCAGAAA  
 AACCATGTCTTTATGCTATAATCATTCCAAATTTGCCAGTGTAAAGTTACAAATGTGGTG  
 TCATTCCATGTTCAGCAGAGTATTTAATTATATTTCTGGGATTATTGCTCTGTCTA  
 TAAATTTGAATGATACTGTGCCTTAATTGGTTTCATAGTTAAGTGTATCATATCAA  
 AGTTGATTAATTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTCCAGATTCAAT  
 CCACCGAAGTGTCACTGTCATCTGTTAGGAAATTTGTTGTCTGTCTTGCCTGGATC  
 CATAGCGAGAGTGTCTGTATTTTAAGATAATTGTATTTGCACACTGAGATATAA  
 TAAAAGGTGTTATCATAAAAAAAAAAAAAA

## **FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRALARRKILFYCHFPDLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKEFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

## FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTT  
 CGCGTTACCTTCTGCTGGCGTTGGAGGCCGTGCTCTACCTCTATCCGGCTTCAGAC  
 AAGCTGCAGGAATTCCAGGGATTACTCCAACGTGAAGAAAAGATGGTAATCTTCCAGATATT  
 GTGAATAGTGGAAAGTTGCATGAGTCCTGGTAATTGCATGAGAGATATGGCCTGTGGT  
 CTCCTCTGGTTGGCAGGCGCCTCGTGGTAGTTGGCACTGTTGATGTACTGAAGCAGC  
 ATATCAATCCAATAAGACATCGGACCCCTTGAAACCAGCTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAATTGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAACCTTGCCCTCCTAAAGCTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTGGTTTGCT  
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG  
 CTTCCAGAAGAATCATGGCACAGTTGGTCTGAGATTGGAAAAGGCTTCAGATGGTCAC  
 TTGATAAAAACATGACTCGGAAAAAACATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTCATTGACTC  
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTG  
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA  
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGCCTGTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGAACTGCCA  
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT  
 CCTAGAGAGACCCTCGTCCTTATGCCCTGGTGTGGACTTCAGGATCTAACACTGGCC  
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGATGAATTAGTAATGAAAACCTTCT  
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTACCC  
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGGAGGGACAGGTATTGA  
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTGGATCACTGTCTCAAAGAGAT  
 ATTAAAATTTCATACATTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTAAAAA  
 AAATCTATGTTGAATCCTTTATAAACCAAGTATCAGTTGTAATATAAACACCTATTGTAC  
 TTAA

## **FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDFETMLKSSLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQE VIRFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL  
QDPNTWPSPHKFDPDRFDELVMKTFSSLGFSGTQECPELRFAYMVTIVLLSVLKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

## **FIGURE 119**

CTAGATTGTCGGCTTGCAGGGAGACTTCAGGAGTCGCTGTCTGAACCTCCAGCCTCAGA  
GACC GCCGCCCTGCCCCGAGGGCC **ATG**GGCCGGGTCTCAGGGCTGTGCCCTTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCGGACAGCAACAT  
ACAGGCCTGCCTGCCTCACGTTCACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGG  
TGGCCCGCTCTGTACCCCTGGGCCTTTGCAGTGGAGCTGGCCGGTTCTCAGGA  
GTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCTCTTCATATTGAGCGTTGGAGTGCACGTACGTATTGGTACATTGGTCT  
TCTGCAGTGCCCTCCAGCTGCACTGAAATGGTTATTGTCACCGTCTTGGGCTGAAA  
AAGAAACCTTC **TGA**TTACCTTCATGACGGAACCTAACGGACGAAGCCTACAGGGCAAGGG  
CCGCTTCGTATTGAGAAGGAAGGCATAGGCTCGGTTCCCTCGAAACTGCTTC  
TGCTGGAGGATATGTGTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATT  
GTGCTTGTAATAAAATGTTGTAGTAACATTAAGACTTATACAGTTAGGGGACA  
ATTAAAAAAAAAAAAA

## FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT  
EMALFVTVFGLKKKPF

### Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

## **FIGURE 121**

TCCCGGACCTGCCGCCCTGCCACTATGTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGGCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCCTGTGCCAGC  
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCGTGGCTGGAACCTCACGGGTGC  
CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTCATGGCAACTACATGG  
ATCGGGTGCCCACACCCAGGCCATCCGGCAGCCCAGGGTCTACTGGCCTGCGGTGGCT  
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGCCACACTACCGCTCCCCTGAGGCC  
CTGCTGATCCGCACCCATTCCCTCCCATGGCAAAACCCACTGTCTCCTCTCCA  
ATAAAGATGTAGCTC

## **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNPASCOQQQARNVQHYHMKTLGWC DVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNPASCOQQQARNVQHYHMKTLGWC DVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

## FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGCTGCTCGTGTTCCTGGTCAGGGTAGCCTATCTGGTATCTGTGCCAGG  
 ATGATGGTCCTCCGGCTCAGAGGACCTGAGCGTATGACCACGAGGGCAGCCCCGGCC  
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGTCAGTCCCAGGCCATTCCACTCT  
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGCATTCTGGCAGCCCCAACGCC  
 CGAACACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTCCAACACAATGCCACAGGCCAGGAAACATCTCCATCAGCC  
 TCGTCCCCCCCAGTAAAGCTGTAGAGTCCACCAGGAACAGCAGATCTTCATCGAACGCAAG  
 GCCTCCAAAATCTCAACTGCCGGATGGAGTGGAGAACGGTAGAACGGGCCGGACCTC  
 GCTTGACCCACGCCAGCCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCCAGCCCTCAAAGTCGTCTGTCTACATCGCCTCTACAGCACGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACATACCATAGTGTACCCCCACTACCCATC  
 TGGG**TGA**CCCAGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCATGC  
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGGTTGGCCTCAGGCAGGGAGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGCCAGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGAATCACAGGAGCACTGGAGGGAGTGGCT  
 CTCTGTGCAGCCTCACAGGGCTTGCCACGGGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGCAGGCCATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAACCCCTGGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGTGGGG  
 CAGAGGAGCTCCAGCCCTGCCTAGTGGGCCCTGAGCCCTTGTGTGCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTCCAAAATCCCTCTGCCAGTACTCCCCCTGTACCAACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAACAGACAGGACGATTGTGGCTCCACACTAACGCC  
 ACAGCCCACCCATCCCGTGCTGTGTCCCTTCCACCCCAACCCCTGCTGGCTCTGGAG  
 CATCCATGTCCCGGAGAGGGTCCCTAACAGTCAGCCTCACCTGTCAAGACCCGGGTTCTCC  
 CGGATCTGGATGGGCCGCCCTCTCAGCAGGGCACGGGTGGGCGGGGGCGCCGCAGA  
 GCATGTGCTGGATCTGTTCTGTGTCTGTGTGGTGGGGAGGGAGGGAAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTGTGTGAAGAACGTCGTGTTCTGGAGCAGGAAATAAGCTT  
 GCCCCGGGGCA

## FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STILLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCVDYNYHSDTPY
YPSG
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA  
 GGCAGGGCTGATTCTGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTAAAG  
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGAATTCAAGCCACAGAAT  
 TGGTGGAAAGTGTGCGCGCCGCCGCGCTCGCTCCTGCAGCGTGTGACCTAGCCGCTAG  
 CATCTTCCCGAGCACCGGGATCCCAGGGTAGGAGGCGACGCAGGGAGCACCAGGCCAGCC  
 GGCTGCGGCTGCCACACGGCTCACC**ATG**GGCTCCGGCGCCGGCGCTGTCCGCGTGGCG  
 GCCGTGCTGCTGGTCTCACGCTGCCGGGCTGCCGTCTGGGACAGAACGACACGGAGCC  
 CATCGTGTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCACGGACTCCAAGG  
 GCTCCTCTCCTCCCCGTGGGATATCGGTCCGGCGGCCACTCCAAGGTGCGCTTCTCG  
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATATTACTT  
 CGATCAGATCCTGGTGAATGTGGTAATTTTCACATTGGAGTCTGTCTTGACCAAGGAA  
 GAAAAGGAATTACAGTTCAAGTTCACTGGTAAAGTCTACAGAGCCAAACTATCCAG  
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTGCGGGGACAAAGATGTTAC  
 TCGTGAAGCTGCCACGAATGGTGCCTGCTCACCTAGATAAAGAGGATAAGGTTACCTAA  
 AACTGGAGAAAGGTAAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT  
 TTCCCCCTA**TAG**GATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG  
 AGTTATTGGAAGATCATTTCATCATTGGATTGATGTCTTTATTGGTTCTCATGGTG  
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTCACAGATTATTGTG  
 TGTGTCTGTTCACTATTTGGATTGGACTCTAACGAGATAATACCTATGCTAAATGTA  
 ACAGTCAAAAGCTGCTGCAAGACTTATTCTGAATTTCATTCCTGGATTACTGAATTAGT  
 TACAGATGTGGAATTTCATTGTTAGTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA  
 AAACTCTAAAGTTCTGACTTCATCACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
 TGTTAAATATATTGATTATTTGTTTATTCCCTTGGATTAGTTGTTGGTTCTGTAA  
 AAAACTGGATTTTTTCAGTAACTGGTATTATGTTCTCTAAAATAAGGTAATGAA  
 TGGCTTGCCCACAAATTACCTTGACTACGATATCATCGACATGACTCTCTCAAAAAAAA  
 GAATGCTCATAGTTGATTTAATTGTATATGTGAAAGAGTCATATTTCAGTTAAGTT  
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAATCTAAG  
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCGAGGGAAATCTTATACTTTATTGC  
 TCAACTTAATTAAAATGATTGATAATAACCACCTTATTAAAAACCTAACGGTTTTTT  
 TCCGTAGACATGACCACTTTATTAACTGGTGGGGATGCTGTTGTTCTAATTATACCTAT  
 TTTCAAGGCTCTGTTGATTGAAGTATCATCTGGTTTGCCTTAACCTTTAAATTGTA  
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATATCTAACATTAGTGCAATAT  
 CTTGTCTTGTATAGGTCAATGAATTCAAAATTATTATGTCTGTTATAGAATAAAGA  
 TTAATATATGTTAAAAAAA

## **FIGURE 126**

MGSRRALSAVPAVLLVLTPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSPLGI  
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIFYFDQILVNNGNFFTLESVFVAPRKGIYSFSE  
HVIKVYQSQTIQVNMLNGKPVISAFAAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

**FIGURE 127**

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTCGGCTGCGCCTCATTGCCTCGGGCTGCGCTC  
GCCCTTATGTCTTACCATGCCATCGAGCCGTTGCGTATCATCTCCTCATGCCGGAGC  
TTTCTTCTGGTGGTGTCTACTGATTGCTCCCTGTTGGTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAAATATCTGCTGATCTTGGAGCGTTGTCTGTC  
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCGACTGCTGGCTATGTTCTGGCT  
TGGGCTTGGAACATGAGTGGAGTATTTCTTGTGAATACCCATCTGACTCCTGGGG  
CCAGGCACAGTGGGCATTCATGGAGATTCTCCTCAATTCTCCTTATTCACTTGGCT  
GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA  
AAAAGTGGGCATCCTCCTATCGTTCTCCTGACCCACCTGCTGGTGTAGCCCAGACCTTC  
ATAAGTTCTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCACTGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTCTTACAACCAGCGCTCCAGA**TAA**CTCAGGGAACCAGCACTCCCAA  
ACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCTTTCTGAAAATCCCTTTCTG  
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 128**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFISSLYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN
FLLYNQRSR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 129**

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTCGCTCTGGGCTTGCCTTCT  
 TGGTGCCTTGGTGGCCTCGTCGAGAGCCATCTGGGGTTCTGGGGCCAAGAACGTCAGCAGAAAGACGCCG  
 AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCAGCTGGTCAACATCTACACCTCAACCATACTGTGACCC  
 GCAACAGGACAGAGGGCGTGCCTGCTGTGAAACGTCCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTGTGG  
 TCCGCCAGAAGGAGGCTGTGGTCTTCCAGGTGCCCCATACTCTGCAGGGATGTTCAGCGCAAGTACCTCT  
 ACCAAAAAGTGAACGAACCCCTGTGTCAGCCCCCAACAAAGAATGAGTCGGAGATTCAAGTCTTCTACGTGGATG  
 TGTCACCCCTGTCACCAGTCACACACATACAGCTCCGGTCAAGCGCATGGACGATTGTGCTCAGGACTG  
 GGGAGCAGTTAGCTCAATACCACAGCAGCACAGCCCCAGTACTTCAGTCAAGTATGAGTCCCTGAAGGCGTGGACT  
 CGGTAAATTGTCAGGTGACCTCAACAAGGCCCTCCCTGCTCAGTCATCTCCATTCAAGGATGTGCTGTGCTG  
 TCTATGACCTGGACAACACGTAGCCTCATCGGCATGTACAGACAGATGACCAAGAAGGGGCCATCACCGTAC  
 AGCGCAAAGACTCCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGCT  
 CCCTGCCTTCTACCCCTCGCAGAAGATGAACCGGTGATCAAGGGCACCGCAGAAAACCTGTCAGTGTGCTGG  
 TGTCTCAAGCAGTCACGCTCTGAGGCATACGTCACTGGGATGCTCTTGCTGGTATATTCTCTCCCTTAC  
 TGCTGACCGTCCCTGGCTGCTGGAGAACCTGGAGGAGAAGAAGAACCCGCTGGTGGCCATTGACCGAG  
 CCTGCCAGAAGCGGTACCCCTGAGTCCTGGCTGATTCTTCTGGCAGTCCCTTATGAGGGTTACAAC  
 ATGGCTCTTGAGAATGTTCTGGATCTACCGATGGTCTGGTGAACAGCCTGGCACTGGGACCTCTCTTAC  
 GTTACCAAGGGCGCTCCTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGATG  
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTGCAACAGCAATACCTCTATGTGGCTGACC  
 TGGCACGGAAGGACAAGCGTGTCTGGGAAAAAGTACCAAGATCTACTCTGGAACATTGCCACATTGCTGTCT  
 TCTATGCCCTTCTGTGGTGCAGCTGTGATCACCTACCCAGCAGCTGGTGAATGTCACAGGAATCAGGACATCT  
 GCTACTACAACCTCCCTGCGGCCACCCACTGGCAATCTCAGCGCTTCAACAAACATCCTCAGCAACCTGGGG  
 ACATCCTGCTGGGCTGCTTCTGCTCATCCTGCAACCGGAGATCAACACACCAACCGGGCCCTGCTGCGCA  
 ATGACCTCTGTGCCCTGGATGTGGATCCCCAACACTTGGGCTTCTACGCCATGGCACAGCCCTGATG  
 TGGAGGGGCTGCTCAGTGTGCTATCATGTGCCCCAATACCAATTCCAGTTGACACATCGTTCATG  
 ACATGATGCCGGACTCTGCATGCTGAAGCTTACCAAGCAGGGCACCGGACATCAACGCCAGCGCTACAGTG  
 CCTACGCCCTGCTGGCATTGTCATCTCTCTGTGCTGGCGTGGTCTTGGCAAGGGAACACGGCGTTCT  
 GGATCGTCTCTCCATCATTACATCGCCACCCGCTCCTCAGCACGCTATTACATGGGCCGGTGG  
 AACTGGACTCGGGGATCTCCGCGCATCCTCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC  
 TCTACGTGGACCGCATGGTCTGGTCACTGGCAACGTCAACTGGTCTGGCTGCTATGGGTTATCA  
 TGCGCCCAATGATTTGCTTCTACTTGTGCTGCAACCTGCTCTTACTTCGCTTCTACA  
 TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTGCACCTCCGTGGTCT  
 GGGGCTCGCGCTCTCTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAAGATCGAGGGAGCACA  
 ACCGGGACTGCATCTCCGACTCTTGACGACCACGACATCTGGCACTTCCCTCCTCCATGCCATGTCG  
 GGTCTTCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAAGGGACAAGATCTATGTCTT**TAGC**  
 AGGAGCTGGGCCCTCGCTCACCTCAAGGGCCCTGAGCTCCTTGTGTCATAGACCGGTCACTCTGCGTGC  
 GTGGGGATGAGTCCCAGCACCGTGGCAGCAGTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTGGCCT  
 GGGACAGCCATGGGGCATGGAAACCTTGCAGCTGCCCTGCGAGGAGCAGGCCCTGCTCCCTGGAACCCCC  
 AGATGTTGGCCAATTGCTGTTCTCAGTGTGGGCTTCCATGGGCCCTGCTTGGCTCTCCATT  
 GTCCCTTGCAAGAGGAAGGATGGAAGGGACACCCCTCCCATTTGCTGCACTTGGCCGTCCTCCCTCCCC  
 ACAATGCCCTGGGACCTAAGGCCCTTCTCCATCTCCACTCCAGGGCTAGTCTGGGCTGA  
 ATCTCTGCTCTGATCAGGCCCTGGGAGGATGAGATTTGGGCTGGCAGCTGGTCTGCAAGCTTGGCTAAGGCTGCAAGGG  
 CCTGGGGCAGTGCCTTCTCCCTGACCTGTGCTCAGGGCTGGCTTCTTAGCAATGCGCTCAGGCCAATT  
 TGAGAACCGCCCTCTGATTCAGAAGGCTGAATTCAAGAGGTCACCTCTCATCCCATCAGCTCCAGACTGATGCC  
 AGCACCAGGACTGGAGGGAGAAGGCCCTCACCCCTTCCCTTCCAGGGCCTAGTCTTGCCAAACCCCC  
 AGCTGGTGGCCTTCAGTGCCTGACACTGCCAAGAACGTCAGGGCAAAAGGAGGATGATACAGAGTTAG  
 CCCGTTCTGCCCTCACAGCTGTGGCACCCAGTGCCTACCTTAGAAAGGGCTCAGGAAGGGATGTGCTGTT  
 CCCTCTACGTGCCAGTCTAGCCTCGCTTAGGACCCAGGGCTGGCTCTAAGTTCCGCTCAGTCTCAGGCA  
 AGTTCTGTGTTAGTCATGCACACACATACCTATGAAACCTGGAGTTACAAAGAATTGCCAGCTGGGAC  
 CCTGCCACCCCTGGCTTGGATCCCCCTCGTCCCACCTGGCCACCCAGATGCTGAGGGATGGGGAGCTCAGG  
 CGGGGCTCTGCTTGGGATGGGAATGTGTTTCTCCCAAACCTGGTTTATAGCTCTGCTGATGGTGCATTCCGTTCTATGAATGAATT  
 TGCATTCAATAACACAGACTCAAAAAAAAAAAAAA

**FIGURE 130**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYDLDNNVAFIGMYQTMTKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTLSQLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVILLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLISYGYQGRSFEPVGTRPRVDSMSSVEEDYDTLDIDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLIIILQREINHNRALLRNDLCALECGIPKHGLFYAMGTALM
MEGLLSACYHVCPTYNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLDSGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDDTVQRDKIYVF

```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

## FIGURE 131

GCTCAAGTGCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTGCTGGCAGCTGGACCAAGGGAGCCAGTCTGGCGCTGGAGGGCCTGTCCTG  
**ACCATGGT**CCCTGCCTGGCTGTGGCTTGTGTCTCCGTCCCCCAGGCTCTCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGGAAGTTCCAGAAAATATGGTGGAAATTCCCTTATACC  
 TGACCAAGTTGCCGTGCCCGTGAGGGGGCTGAAGGCCAGATCGTGTCAAGGGACTCA  
 GGCAAGGCAACTGAGGGCCCATTGCTATGGATCCAGATTCTGGCTTCTGCTGGTACCCAG  
 GCCCTGGGACCGAGAGGAGCAGGCAGAGTACCAAGCTACAGGTACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGTCCACAGCCTGTGCTGTGACGTGAAGGATGAGAATGACCAAGGTG  
 CCCATTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACCAAGGCCTGGCATCCC  
 CTTCTCTTCTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTGACCACGCCCTGGAGAGGAC  
 CTACCAAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGCTCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCTTACACCGCACCACATGCCAGGTACACTGGAGTGGGGTGTGATGT  
 GCACTATCACCTGGAGAGCCATCCCCCGGACCCCTTGAAGTGAATGCAGAGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAACGCCAGGCTGAGTACCTGCTCCAGGTGCAGGGCTCAG  
 AATTCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTATGGATGAGAA  
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGAAGTGAAGACTGAGCAGAGGATGCAAGATGCCCGGCTCCCCAATTCC  
 CACGTTGTGATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGGAGAGCCTTCCA  
 GGTGGACCCCACCTCAGGCACTGTGACGCTGGGGTGCTCCACTCCAGCAGCAGGCCAGAACAA  
 TCCTGCTCTGGTGCCTGGCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
 GAAGTCGAAGTCGCACTGAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGAT  
 TGGCCTATAAGCCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCGCCCTCCGCCTCATGGATTTCGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTGGCCTGGATTGGAGCCAGACTCTGGGATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCAAGTCATGAGGTGGGGTGCTGGAGAGTGTGGCGA  
 AGCTGGTGGGCCAGGCCAGGCCCTGGAGCCACGCCACGGTACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGGCC  
 AGCCGGCTTTCTGCTGACCATCCAGCCCTCCGACCCATCAGCCGAACCCCTCAGGTTCT  
 CCCTAGTCATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC  
 GCCCAGTCCCTGCAGGGGCCAGCCTGGGACACCTACACGGTGTGTTGGAGGCCAGGA  
 TACAGCCCTGACTCTGCCCTGTGCCCTCCCATACCTCTGCACACCCGCCAAGACCATG  
 GCTTGATCGTGAAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGCACGGTCCCTACAGC  
 TTCACCCCTGGTCCCAACCCACGGTGCACGGGATTGGCGCCTCCAGACTCTCAATGGTTC  
 CCATGCCTACCTCACCTGGCCCTGCATTGGTGGAGGCCACGTGAACACATAATCCCGTGG  
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCTGGTCAGTGATCGTGTGCGCTGCAAC  
 GTGGAGGGCAGTGCATGCGCAAGGTGGCCGCATGAAGGGCATGCCACGAAGCTGCGGC  
 AGTGGGCATCCTGTAGGCACCCCTGGTAGCAATAGGAATCTCCTCATCCTCATTTCACCC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTCCCCCTGAAGGCG  
 ACTGT**TGA**ATGGCCCAGGCAGCTAGCTGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAAGGTGCTGCAGAGCCTGGACACCAAC  
 TTTATGGACTGCCCATGGAGTGCTCCAAATGTCAAGGGTGTGCTGGCCAATAATAAGCCCCA  
 GAGAACTGGCTGGGCCATGGAAAAAAAAAAAAAAAG

## **FIGURE 132**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
 KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHKDENDQVP  
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPD MFQLEPRL  
 GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSIESTWV SLEPIHLAE  
 NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN  
 SHGEDYAAPPLELHV LVM DENDNV PICPPRDPTV SIPELSPPGTEVTRL SAEDADAPGSPNSH  
 VVYQLLSPEPEDGV EGRAFQVDPTSGSVTLGV LPLRAGQ NILLVLAMDLAGAEGGFSSTCE  
 VEVAVTDINDH APEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTE  
 GTFGLDWE PDSGHV RLCKNLSYE AAPSHE VVVVVVQSVAKL VGP GP GPGATATVTVLVERV  
 MPPP KLDQESYE ASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWL CIEKF SGEVHTA  
 QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLC TPRQDHGLIVSGPSKDPDLASGHGPYSF  
 TLGP NPTVQRDWRLQTLNGSHAYLT LALHWV EPREHIIIPVVVSHNAQM WQLLVRVIVCRCNV  
 EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFT HWTMSRKKD P DQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## **FIGURE 133**

CCGGGGAC**ATG**AGGTGGATACTGTTATTGGGCCCTATTGGTCCAGCATCTGTGGCAA  
 GAAAAATTTTGGGGACCAAGTTGAGGATAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTCTGGAAATCTCCCTCCT  
 TCAATCGGCCTGTGGATGTCCTGGTCCCCTGTCACTGCAGGCATTAAATCCTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAATGA  
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTCAACTACGGGG  
 CTTACCATTCCCTGAAAGCTATTACACAGAGATGGACAAACATTGCCAGACTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGGCCTGAGGCGGCCGCTTGGCTGAATGCAGGCATCCATTCCGAG  
 AGTGGATCTCCAGGCCACTGCAATCTGGACGCCAGGAAGATTGTATCTGATTACCAGAGG  
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTTCCTGTTGCCGTGGCAAATCC  
 TGATGGATATGTGTACTCAAACCTCAAACCGATTATGGAGGAAGACGCCGTCCGAAATC  
 CTGGAAAGCTCCTGCATTGGTGTGACCCAAATAGAAACTGGAACGCTAGTTGCAGGAAAG  
 GGAGCCAGCGACAACCCCTGCTCCGAAGTGTACCATGGACCCCACGCCAATTGGAAGTGG  
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGAATTCAAGGGCTCATGCACCTGC  
 ACAGCTACTCGCAGCTGTGATGTATCCATATGGGTACTCAGTAAAAAGGCCAGATGCC  
 GAGGAACCTCGACAAGGTGGCGAGGCTGGCCAAAGCTCTGGCTTCTGTGTGGCACTGA  
 GTACCAAGTGGTCCCACCTGCACCACTGTCTATCCAGCTAGCAGGAGCAGCATGACTGG  
 CGTATGACAACGGCATCAAATTGCAATTGATTGAGTTGAGAGATACGGGACCTATGGC  
 TTCCCTGCCAGCTAACCATCATCCCCACTGCAGAGGAGACGTGGCTGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTACT**TAG**CGATGGCTCTGCTCTGTCTACATTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGAAAGGAGCTTTCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTGTGGAGCACACAGGCCTGCCCTCTCAGCCAGCTCCCTGGAGT  
 CGTGTGCTGGCGGTGTCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTGGTCTG  
 CTGTTTTGATGAGCCTTGTCTGTTCTCCACCTGCTGGCTGGCGCTGCACTC  
 AGCATCACCCCTCCTGGTGGCATGTCTCTACCTCATTAGAACCAAAGAACATC  
 TGAGATGATTCTCTACCCATCCACATCTAGCCAAGCCAGTGAACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCAACTGTCTTAGGTGGTCTCAAAGATGATGTAGAACATTCTCTTAATT  
 TCGCAGTCTCCTGGAAAATATTCTCTTGAGCAGCAAATCTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCCTGTTTTTTGAGACAGAGTTGCTTGTGCTTGTGCT  
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACCACAACTCTGCCCTGGGTTCAAGCA  
 ATTCTCCTGCCCTCAGCCTCTTGAGTAGCTGGTTATAGGCGCATGCCACCATGCCCTGGCTA  
 ATTGTTGTTTTAGTAGAGACAGGGTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA  
 ACCTCAGGTGATCTGCCCTCCTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCCGTCCCTCTTTAGGCCTGAATACAAAGTAGAGATCAGTGTGCT  
 TGTGCTGAGAATTCTAGATACTACAGTCTTACTCCTCTCTCCCTTGTATTCAAGTGT  
 ACCAGGATGGCGGGAGGGATCTGTGTCAGTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTGAGGATGGTGAATTATCCCCATCTGCTTAATGGGCTTACCTCCT  
 CTTGCCTTTGAACACTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCATTGCTGTGTGTGTGTTGTGTT  
 TCCCTGCTGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTT  
 TCTGTCTATTGATCCTGGACCAAGTCTAAAGTAGAGCAAGAACATTCAACCAGCT  
 GCCTCTGTTCAATTACACCTCAGCACGTACCATCTGCTCTTGTGTTGTGTT  
 TTGTTTTTGCTTACAAACATGTCTGAAATCTAACCTCCTGCCTAGGATTGTACA  
 GCATCTGGTGTGCTTATAAGCCAATAATATTCAATGTGAAAAA

## **FIGURE 134**

MRWILFIGALIGSSICGQEKFQGDQVLRINVNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAWVLNAGIHSREWI  
SQATAIWARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY  
SQLLMYPYGVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPPTAEETWLGLKTIMEHVRDNLY

**Signal peptide:**

amino acids 1-16

## **FIGURE 135**

## **FIGURE 136**

MASYLYGVLFAGVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFPSPSVSTSLAMLSLGAHSVTKTQILQGLGFNLHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYAEVFSTDFSNPSIAQARINSHVKKKTQGK  
VVDDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDAVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSDLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

## FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAACCGAAGGCATCCAGCTGCCACGC  
 CTGAGTCCAAGATTCTCCCAGGAACACAAACGTAGGAGACCCACGCTCTGGAAGCACCAG  
 CCTTTATCTCTCACCTCAAGTCCCCTTCTCAAGAACATCCTCTGTTCTTGCCTCTAAAG  
 TCTTGGTACATCTAGGACCCAGGCATCTGCTTCCAGGCCACAAAGAGACAG **ATGAAGATGC**  
 AGAAAGGAAATGTTCTCCTTATGTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC  
 AATGAGACTAGCACCTCTGCAACACTGGATCCAGTGTGATCTCAGTGGAGCCAGCACAGC  
 CACCAACTCTGGGCCAGTGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCA  
 GCGTACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGG  
 ATCAGCACAGCCACCAACTCTGAGTTAGCAGCACAGCGTCCAGTGGGATCAGCATAGGCCACAA  
 CTCTGAGTCCAGCACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC  
 CCTCCAGTGGGCCAGCACAGTCACCAACTCTGGTCCAGTGTGACCTCCAGTGGAGGCCAGC  
 ACTGCCACCAACTCTGAGTCCAGCACAGTCAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA  
 GTCTAGCACACTCTCCAGTGGGCCAGCACAGCCACCAACTCTGACTCCAGCACACCTCCA  
 GTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCACAGCC  
 ACCAACTCTGAGTCCAGCACAGTCAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG  
 CACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGG  
 CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAAC  
 TCTGACTCCAGCACAGTCAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC  
 CTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCTAGCA  
 CAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCGGCACAGCCACCAACTCTGAG  
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAG  
 TGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCA  
 CCAACTCTGAGTCCAGCACAGTCAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGC  
 ACAACCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGG  
 TAGCACAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGTGAGGCCAGCACAGCCACCAACT  
 CTGAGTCTAGCACAGTCAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAAAC  
 TCCAGTGGGCCAACACAGCCACCAACTCTGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC  
 AGCAGCTCTGACTGGAATGCACACAACCTCCCAGTGCATCTACTGCAGTGAGTGAGGCAA  
 AGCCTGGTGGTCCCTGGTGGCAAGGGAAATCTTCCATCACCCCTGGTCTCGGTTGTGGCG  
 GCCGTGGGCTTTGCTGGCTCTCTGTGAGAAACAGCCCTGTCCCTGAGAAACAC  
 CTTAACACAGCTGTCTACCACCCATGGCCTCAACCAGGCCTGGTCCAGGCCCTGGAG  
 GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCCTAACTGGTTCTGGAGGAGACAGTA  
 TCATCGATGCCATGGAGATGAGCGGGAGGAACAGCGGGCCC **TGA**GCAGCCCCGGAAAGCAAG  
 TGCCGCATTCTCAGGAAGGAAGAGACCTGGCACCCAGACCTGGTTCTTCATTCTCATC  
 CCAGGAGACCCCTCCAGCTTGTGAGATCTGAAATCTGAGAAGGTATTCCCTCACC  
 TTTCTGCCTTACCAAGACACTGGAAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA  
 ATACATCTCATCTAACACACAGACAAAGAGAAGCTGTGCTGCCCCGGGTGGGTATCTAG  
 CTCTGAGATGAACTCAGTTAGGAGAAACCTCCATGCTGGACTCCATGGCATTCAAAA  
 TCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAA

## **FIGURE 138**

MKMQKGNVLLMFGLLHLEATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI  
SGSSVTSGVSIVTNSEFHTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSE  
SSTPSSGASTVTNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTT  
SNGAGTATNSESSTSSGASTATNDSSTVSSGASTATNSESSTSSGASTATNSESSTTSS  
GASTATNDSSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTSSGVSTATNSESSTSSGASTATNDSSTTSEAST  
ATNSESSTVSSGISTVTNSESSTSSGANTATNGSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGLVPWEIFLITLVSVVAAVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAPHRPRWSPNWFWRPVSSIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTCCCTGGCTCCTCTGCATCCTCCGACCTTC  
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTCTGCTACTGGGGGCC  
CTGTCTGGATGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
ATGCCGGAAGGGAAAGTGGAGAAGGTTCAACGGACTTAGCAACATGGGAGGCCACACCGGC  
AAGGAGTTGGACAAAGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAAACTTGGCAAGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
TGCAGAATGCTCATATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG  
GCCCTCAGTCAACACGCCCTTCATCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCTAAAACTGGCATCCGGCCTTGCTGGAGAATAATGTCGCCGTTGTACATCAGCTGAC  
ATGACCTGGAGGGTTGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGTTGTACTG  
GGATTTGTGAATAACTTGATACACCA

## **FIGURE 140**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLQGVNHAADQAGKEVEKLQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTPLASGVNTPFINLPALWRSVANIMP
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

## FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGGCGGCCCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC  
 CCCCGGGGGGCGATGACCGTGCCTGACTCACCTCAGGTCGGAGGCGGGGGCCCCGGGGACTCG  
 GGGCGGGACCGCGGGGGCGAGCTGCCGCCGTGAGTCGGCCGAGCCACCTGAGCCCCGAGCCGGACACCGTC  
 GCTCCTGCTCTCCGA**ATG**CTGCGCACCGCGATGGGCTGAGGAGCTGGCTCGCCGCCCTGGACCTGGCGCTGCC  
 CCTCGGCCACCGCTGCTGCTCTGCTGCTGCTCAGCTGCCAGCAGATTGAAGCTGAACACATCTCAACTAC  
 CCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGAAGCTGAACACATCTCAACTAC  
 ACAGCCCTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTTGTGACTCAGTAGC  
 AACCTCAGCTTCTGCCAGGGGAGTACCAAGGAGCTGCTTGGGTGAGACGAGAAGAAACAGCAGTG  
 AGCTTCAAGGGCAAGGACCCACAGCGGACTGTCAAAATACATCAAGATCCTCTGCCGCTCAGCGCAGTCAC  
 CTGTTACACTGTGGCACAGCAGCCTCAGCCCCATGTGACCTACATCAACATGGAGAACTTCAACCTGGCAAGG  
 GAGGAGAAGGGGAATGTCTCTGGAAGATGGCAAGGGCGTTGTCCCTCGACCCGAATTCAAGTCCACTGCC  
 CTGGTGGTGTGGCGAGCTTACACTGGAACAGTCAGCAGCTTCCAAGGGGAATGACCCGCCATCTCGCGGAGC  
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTGTGGCCTCAGCCTAC  
 ATTCCCTGAGAGCCTGGGAGCTTGAAGGCGATGATGACAAGATCTACTTTTCTCAGCGAGACTGCCAGGAA  
 TTTGAGTTCTTGAGAACACCATTGTGTCCTGCATTGCCGATCTGAAGGGCGATGAGGGTGGAGAGCGGGTG  
 CTACAGCAGCGCTGGACCTCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTTCCCTCAAC  
 GTGCTGAGGATGTCCTCACGCTGAGCCCCAGCCCCAGGACTGGCGTGAACCCCTTCTATGGGGTCTTCAC  
 TCCCAAGTGGCACAGGGAAACTACAGAAGGCTCTGCCGCTGTGCTTCAATGAAGGATGTGAGAGACTTTC  
 AGCGCCCTCTACAAGGAGGTGAACCGTGGAGACACAGCAGTGGTACACCCTGACCCACCCGGTGCCACACCCGG  
 CCTGGAGCGTGCATACCAACAGTGGCCGGAAAGGAAGATCAACTCATCCCTGAGCTCCAGACCGCGTGTG  
 AACCTCTCAAGGACACTTCTGATGGACGGCAGGTGCGAGCCGATGCTGCTGCTGAGCCCGAGGCTCGC  
 TACAGCGCGTGGCTGTACACCGCGTCCCTGGGCTGACACACCTACGATGTCCTCTTGTGGCAGTGGTGAC  
 GGCGGCTCCACAAGGCACTGAGCGTGGGCCCCGGGTGACATCATTGAGGAGCTGAGATCTCTCATCGGGA  
 CAGCCCGTGCAGAATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCCGCTCACACTCGGGCGTAGTCCAG  
 GTGCCCATGGCAACTGAGCCTGTACCGGAGCTGTGGGACTGCTGCCCTCGCCGGGACCCCTACTGTGCTTGG  
 AGCGGCTCCAGCTGCAAGCACGTCAAGCCTCTACAGCCTCAGTGGGACCCAGGGCTGGATCCAGGACATCGAG  
 GGAGCCAGCGCCAAGGACCTTGAGCGCTTCGGTTGTGTCCCCGTCTTGTACCAAACAGGGGAGAAGCCA  
 TGTGAGCAAGTCCAGTCCAGCCAAACACAGTGAACACTTGGCTGCCGCTCTCTCAAACCTGGGACCCGA  
 CTCTGGCTACGCAACGGGCCCCGTCAATGCTCGGCCCTGCACTGGCTACCCACTGGGACCTGCTGCTG  
 GTGGGACCCAAACAGCTGGGGAGTCCAGTGTGGTCACTAGAGGAGGGCTCCAGCAGCTGGTAGCCAGCTAC  
 TGCCCAGAGGTGGAGGACGGGTGGCAGACCAAACAGATGAGGGTGGCAGTGTACCCGTATTATCAGCACA  
 TCGCGTGTGAGTGCACCAGCTGGTGGCAAGGCCAGCTGGGTGAGACAGGTCTACTGGAAGGAGTCTGGT  
 ATGTGACGCTTTGTGCTGGCGTGCTGCTCCAGTTTATTCTGCTTACCGGCACCGGAACAGCATGAAA  
 GTCTCCTGAAGCAGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGCTGCCCTGAGACCCGC  
 CCACTCAACGCCCTAGGGCCCCCTAGCACCCGCTCGATACCGAGGGTACAGTCCCTGTCAGACAGCCCCCG  
 GGGGCCGAGTCTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTCGTGGAGGTATCCCTG  
 TGCCCCCGGGCCCCGGGTCCGCTTGCTCGAGATCCGTGACTCTGTGGTG**TGA**AGAGCTGACTTCCAGAGGACG  
 TGCCCTGGCTTCAAGGGCTGTGAATGCTCGAGGGTCAACTGGACCTCCCTCCGCTCTGCTTCTGGGAAC  
 ACGACCGTGGTGGCCGGCCCTTGGGAGGCTGGAGGCCAGCTGGCTGCTCTCCAGTCAGTAGCGAAGCTCC  
 TACCAACACACCCAAACAGCGTGGCCAGAGGTCTGGCAAATATGGGGCTGCTAGGTTGGTGAA  
 CAGTGTCTTATGTAAACTGAGCCCTTGTGTTAAAAACAAATTCCAATGTGAACACTAGAATGAGAGGGAGAG  
 ATAGCATGGCATGCAGCACACAGCGTGTCCAGTTCATGCCCTCCAGGGTGCTGGGATGCATCCAAGTGG  
 TTGCTGAGACAGAGTTGAAACCCCTACCAACTGGCCTTCCACCTTACATTCCGCTGCCACCGGCTG  
 CCTGCTCACTGCAAGATTCAAGGACAGCTGGCTGCGTGTGCTGCCAGTCAGCCAGGATGTAGTTG  
 TTGCTGCCGTGTCCTCACCTCAGGGACCAAGAGGGCTAGGTTGGCACTGCCCTCACCAAGGCTGGGCTC  
 GGACCCAACCTGGACCTTCCAGGCTGTATCAGGCTGTGGCCACAGCAGAGGGAGACGCGGAGCTCAGGAGAGA  
 TTCTGACAATGTACGCCTTCCCTCAGAAATTCAAGGGAGAGACTGTCGCTGCCCTCCCTGGTTGCGTG  
 GAACCCGTGTGCCCTTCCCACCATATCCACCCCTGCTCCATCTTGAACACTCAAACACGAGGAACACTAAC  
 CTGGCTCTCCCCAGTCCCCAGTTACCCCTCACCTTCCACTCTAAGGGATATCAACACTGCC  
 AGCACAGGGCCCTGAATTATGTGGTTTATACATTAAAGATGCACCTTATGTCAATTAAATAAAA  
 GTCTGAAGAATTACTGTTAAAAAAAAAAA

**FIGURE 142**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLL LLLL LLLL QPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRSQSLRPTKTESSLNWLDQPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFILMDGQVR
SRMLLQPOQARYQRVAVHRVPGLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSPLYQP
QLATRPWIQDIEGASA KDLCSASSVVSFSVPTGEKPCEQVQFQPNTVNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDL LLLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSPVIIISTSRVSAPAGGKASWGADRSYWK EFLVMCTLFVLAVLLPVLFL YRHRNSM
KVFLKQGECASVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFT ESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

```

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

## **FIGURE 143A**

CTAAGCCGGAGGATGTGCACTGCGGGCGGGCGGGCTACGAAGAGGACGGGGACAGGCCTCGTGCAGACCGA  
GCCCAGCCAGCCGGAGGACCGGGCAGGGAGCCGGACTCGTCTGCCGCCGCGCTGCCCTCG  
TGCGGGCCCCCGCTCCCCCGCGCAGCGGGAGGAGCCGCCACCTCGCGCCGAGCCGCCCTAGCGCGC  
CGGGCATGGTCCCCCTCTAAAGGCGCAGGCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
CCTGCAGGGCGGCTCGGGGGCGCGATGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
CGGCGCTAGGGCGGCTGGCTCCGTGGCGGGGGCAGCGGGCTGAGGGCGCGGGAGGCCCTGCCGCCG  
GGCGGGCGGCCGG  
ATGCGCGCGCGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC  
TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCTCGCGCTCGTCTGCCCGGGCTTCCAGGCCGCCGCCGCCGCC  
GCCCACGGCGCCGCCAGCCCCGAGGGCTGCCGGTCCGGGAGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC  
GCGATGCGCGCGGGCGCAGCTCTGCCGCCGCCAGATGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC  
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGCCGTGGCGCCTACAGAACATGGTCAAGAACAA  
TTCTGGGAAAGTCTAGTTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCCAGTAGGCCACTACGGG  
GTGTGGGAGCACTCTACCCGCCAGAAGAACAGTCCTCATGATGCTCAAGTACATGCCACCAACTTGGACA  
AGTATGAATGGTTATGAGAGCAGATGATGACGTACATCAAAGGAGACCGTCTGGAGAACTCCTGAGGAGTT  
TGAACAGCAGCGAGCCCTCTTCTTGGGAGACAGGCCCTGGGACCCAGGAAGAAATGGGAAACTGCCCTGG  
AGCCTGGTGAAGAACTTCTGCATGGGGGGGCTGGCGTGAATGAGCCGGGGAGGTGCTCGGAGAACGGTCCG  
ACATTGGCAAGTGTCTCGGGAGATGTACACCAACCATGAGGACGTGGAGGTGTGCTGGAGGTTTG  
CAGGGGTGAGTGTCTGGCTTATGAGATGCCAGCTTGTGAGGAGATGCCAGCTTGTGAGGAGGTTTG  
ACATTAGAGATCTCATAACAGTAAATCAGCTACATTACACCCAAACAAAAACCCACCCCTACCAAGT  
ACAGGCCTCCACAGCTACATGCTGAGCCCAAGATATCCGAGCTCCGCACTGCCACAAATACAGTGCACCGCGAA  
TTGTCTGATGAGCAAATACAGCAACACAGAAATTCTAAAGGAGGACTCCAGCTGGGAATCCCTCCCTCTCA  
TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGAGTTCTGACTGGAAAATACTGTATTGGCAG  
TTGACGCCAGCCCCCTGAAAGAGGAATGGACTCCGCCAGGGGAAGCCTTGGAGACATTTGATGCAAGGTCA  
TGGAGATGATCAATGCCAACGCCAGACAGGGCGCATATTGACTTCAAGAGATCCAGTACGGCTACGCC  
GGGTGAACCCATGATGGGCTGAGTACATCTGGACCTGCTCTGTACAAAAGGACAAAGGGAAAGAAAA  
TGACGGCCCTGTGAGGAGGACCGCTATTACAGCAGACTTCAGCAAATCCAGTTGTGGAGCATGAGGAGC  
TGGATGACAAGAGTTGGCCAAGAGAAATCAATCAGGAATCTGGATCTTGTCTTCTCTCAAACACTCCGAGA  
AGCTCGCCCCCTTCAGCTCCGTGGCGAAGAGTGACCAAGAACCAAGATAAAAGATAAACATACTGA  
TTCCTTGTCTGGCGTTGACATGTTGTGAGATTATGGAAACTTGAGAAGACGTGTCTATCCCCAATC  
AGAACGTCAGCTGTGGTTCTGTTCAATTCTGACTCCAAACCTGACAAGGCCAACAGTGAACGTGATGA  
GAGATTACCGCATTAAAGTACCTAAAGCCGACATGCAAGATTGCTGTGCTGGAGAGTTCAAGGCCCTGG  
CCCTGGAAGTAGGATCCTCCAGTTAACATGAATCTTGTCTTCTCTGCGACGTGACCTCGTGTACTA  
CAGAATTCTCAGCGATGTCGAGCAAATACAGTCTGGCCAACAAATATTTCAATCATCTCAGCCAGT  
ATGACCCAAAGATTGTTATAGTGGAAAGTCCAGTGACAACCATTGCTTACTCAGAAAATGGCTCT  
GGAGAAACTATGGTTTGGCATCACGTGATTATAAGGGAGATCTGCTCGAGTGGTGGCTTGATGTTCCA  
TCCAAGCTGGGGCTGGAGGATGTGGACCTTTCAACAAAGGGTGTCCAGGCAGGTTGAAGACGTTAGGAGCC  
AGGAAGTAGGAGTAGTCACGCTCCACCATCCTGTCTTGTGATCCAAATCTTGACCCCCAACAGTACAAATGT  
GTTGGGGTCCAAAGCATCGACATTGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCA  
GTTACAGTAAAGCAGCAATAATAGGCTCAGTGAGGACAGCC**TAA**TGTCAGCTTGTGGAAAAGACGTTT  
TAATTATCTAATTATTTCAAAAATTGGTGTGAGATTGATCAGTTTGAGTCCGTATAAGGAGATATTGAA  
AAGTGGTTTCTTACATAGGACTCCTTAAGATTGAGCTTCTGAAACAAGAAGGTGATCAGTGTGTTGCCCTTGAA  
CACATCTCTGCTGAACATTATGAGCAGACTGCTTAACTTGAGTAACTGACCTGATGAGAACAAAATTT  
TTTAAAAAAATGTTTCTTTGAGACCTTGTCTCAGTCTATGGCAGAAAACGTGAACATTCTGCAAACAT  
TATTGTAACAAAACACTGTAACTCTGGTAAATGTTGTGATTGTTAACATTCCACAGATTCTACCTTTGT  
GTTTGTGTTTTTACATTGTTAAAGCCTATTGATGTTCAAGTGAAGATAAGGAAATGTGATAATA  
GCTGTTCATATTGTCAGGAGAGCTTCCAGGTTGATCATTCTCTCATGGTACTCTGCTCAGCATGGC  
CACGTAGGTTTGTGTTGTTGTTCTTGTGAGACGGAGCTCACTCTGTTACCCAGGCTGGAAATG  
CAGTGGCGCAATCTGGCTCAGTTAACCTCCACTCCCTGGTCAAGCAATTCCCTGCCCTTGCTCCGAGT  
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTGTGTTAGTAGAGACGGGTTTACCAT  
GCAAGCCAGCTGGCACGTAGGTTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGGTTATGTTGCTGTTCTG  
TGGTAGTTCATCGGCCAAATAGACCTGGCATTAAATTCAAGAAGGATTGGCATTCTCTGACCCCT  
CTCTTTAAAGGGTAAATATTAGTTAGAATGACAAAGAGTGAATTATTACAATAATCTGATGTCACAGACT  
GAAACATACACACATACACCCCTAATCAAAACGTTGGGAAAAATGATTGGTTTGTCTTACCTGCTG  
TGTGTTAGTGTGGTGGAGATGGTTTCTTCAATTACTGTTGTTATCCTTGTATCTGAAATACTTAA  
TTTATTAAATATCTGTTGTCAGAGCTGCCATTCTGAGTACCTGTTAGTAGTATTATTATGTGATCGG  
GAGTGTGTTAGTCAGTGTGTTATTGCAAGAACGATCTCCAAAGATTCCCTTTGAAACGCTTTCCCTCC

**FIGURE 143B**

TTAATTTTATATTCTTACTGTTACTAAATATTAAGTGTCTTGACAATTGGTGCATGTGTTGGG  
GACAAAAGTGAATGAATCTGTCATTATACAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT  
TTCATTTAGATTCAAACAGTGATAGACTGCCATTAAATACACGTCATTGGAGGGCTGCGTATTGTAAATAG  
CCTGATGCTCATTGGAAAAATAAACAGTGAAACAATATTTCTATTGACTTTGAACCATTGTCTCATT  
ATTCCCTGTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

**FIGURE 144**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRRAWLSVLLGLVLFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPPIPVLGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRAADDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQQY
GYRRVNPMYGAEYILDLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSLNSLKKLVPFQLPGSKSEHKEPKDKKINILIPSLGRFDMFVRFMGNFEKTC
LIPNQNQNVKLVVLLFNNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEDVDFNKKVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCIGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

```

**Signal peptide:**

amino acids 1-23

## FIGURE 145

GGACAAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACACCTTCCC  
 TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
 ACGGACGACGCCTATGAAGCCCTTAGTCCTCTAGTTGCGCTTGTATGGCCTCGTCTG  
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTTGAATCATTATATA  
 CAAGTTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC  
 TAACTCTCCAAAACATGTTATTCTATAGCATCAAAGGGATCAAATTAAGGAGCTAGTTA  
 CACATGGAGACGCTCAACTGAGAATGATGTTAACCAATCCTATCAGTGAAGAAACTACA  
 ACTTCCCTACAGGAGGCTTCACACCGAAATAGGAAAGAAAAACACACGGAAAGTACCCC  
 ATTCTGGTCGATCAAACCAAACATGTTCCATTGTTGCATGCAGAGGAACCTTATATTG  
 AAAATGAAGAGGCCAGGCCAGGCCAGCTGCACAAACTGAGGCACCAAGAATG  
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC  
 CACTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
 CAGGTGAAACTGCGATAGAAAAACCGAAGAGTTGAAAGCACCCAGAGAGTTGGAATAAT  
 GATGACATTGAAAAAAATTAGATATTAATTACAAGTGCAACAGGCACCTCTAGTGA  
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCC  
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACATGTATAAGTCCAGTTATTGCCA  
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGAATTG  
 TAGATCTAAACTCTATGAATATTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG  
 CTGCTACAGTATTCAATACATTAAAAATATGTGAGATCAAGGAGAGTCACAGCCTTATTA  
 AAAGTTATTAAACAATAATATAAAATTAAACCTACTGATATTCCATAACAAAGCTGA  
 TTTAAGCAAACGCATTTTCACAGGAGAAATAATCATATTGTAATTCAAAAGTTGTAT  
 AAAAATATTCTATTGAGTCAAATGTGCCAACATCTTATGTGTCATGTGTTATGAACA  
 ATTTCATATGCACTAAAAACCTAATTAAAATTTGGTTCAGGAAAAAA

## **FIGURE 146**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pi: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTFPTGGFTPEIGKKKTESTPFWSI
KPNNVSIVLHAEPYIENEPEPEPEPAAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAEEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

**Signal peptide:**

amino acids 1-19

## FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCAAATCATCCATCCACCCCTGCTGTATCTGTTTCACTAGTGTGAGATCAACCCACA  
 GGAATATCC**ATG**CTTGTGCTCATTTGGTTCTCAGTTCTACAGCTGGTGTAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTCCGTAGAGACCAGTCAGAGGCTATGGAAGTGCCTCTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTACAGAGATGGGAAGACTGGGAATCTAACAGATGCCACA  
 GTATCGAGGGAGAACTGAGTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAACAGC  
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTCAAGTCCCAGATTAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGTGGCAGCACTGGCTCACTCCCTCTCATTCCAT  
 CGTGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTCCCCCAGC  
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTTCAGACTCCAGAGCAAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCATTATAGTCAGGAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTCCAGCCCTCACCTGGCGCTGGCTCTATTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTCATGGGATGATAATTGTTTCTTCAAATCCAAGGGAAAATCCA  
 GCGGAACTGGACTGGAGAAGAACGGACAGGCAGAATTGAGAGACGCCGGAAACACG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCTGCCTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCCAGGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA  
 GAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGAGGTGGACGTGGGAC  
 AAAATGTAGGGTGGTATGTGGAGTGTGTCGGATGACGTAGACAGGGGAAGAACATGTG  
 ACTTTGTCTCCCAACAATGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTCAC  
 ATTCAATCCCCATTATCAGCCTCCCCCCCAGCACCCTCCTACACGAGTAGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTCTTCAATAACAAATGACCAAGTCCCTTATTATACC  
 CTGCTGACATGTCAGTTGAAGGCTTGTGAGACCCCTATATCAGCATGCGATGTATGACGA  
 GGAAAAGGGACTCCCATTATCATATGTCAGTGTCTGGGG**TGA**GACAGAGAACCCCTG  
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGC  
 CCCAGCTCTCTCCGGAGCCTGCGCACAGAGACTCACGCCCTACTCTCCTTAGGGAGC  
 TGAGGTTCTCTGCCCTGAGCCCTGAGCAGCAGGGCAGTCACAGCTCCAGATGAGGGGGAT  
 TGGCCTGACCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGAGGAATAGACTCA  
 CATTAGTTTAGTTGTGAAAACCTCCATCCAGCTAACGATCTGAACAAAGTCACAACCTCC  
 CAGGCTCCTCATTGCTAGTCACGGACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGA  
 CAACGAATGTGAATCATGCTGAGGTTGAGGGCACAGTGTGCTAATGATGTGTTTTA  
 TATTATACATTTCCCACCATAAACTCTGTTGCTTATTCCACATTAATTACTTTCTCTA  
 TACCAAATACCCATGGAATAGTTATTGAACACCTGCTTGTGAGGCTCAAAGAATAAGAG  
 GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG  
 AAAACAGAAGAAGAGGAAGGAAAATACAGGTCCATATCCCTCATTAACACAGACACAAAAA  
 TTCTAAATAAAATTAAACAAATTAAACTAAACAAATATTTAAAGATGATATATAACTACT  
 CAGTGTGGTTGTCCACAAATGCAGAGTTGGTTAATATTAAATATCAACCAGTGTAAATT  
 CAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

## FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pi: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKVFQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQOPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVASQGFQAGRHYWEVDVGQNVGVYVGVCRDDVDRGKNNVTLS
PNNGYWVRLLTTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTGTTGGAACCCCTGGGTTATCGGCCTCGTCATCTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTCAATTATGTGAGATATAATCAAAAGAAGACCTACAA  
 TTACTATAGCACATTGTCATTACAACGTACAAACTATATGCTGAGTTGGCAGAGAGGCTT  
 CTAACAATTTACAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAA  
 TCTCCATTAAGGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAAGTCAACAGAACATGG  
 AGTGTGGCTCATATGCTGTTGATTGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
 ATAAAATTGTTCAACTTGTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTA  
 GATCCTCACTCAGTTAAAATTAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAAACCTCTAGGTAGAGTCTCAGGATCGTTGGTGGACAG  
 AAGTAGAAGAGGGTGAATGCCCTGGCAGGCTAGCCTGCAGTGGATGGAGTCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTACAACATATAA  
 GAACCCCTGCCAGATGGACTGCTCCTTGGAGTAACAATAAAACCTCGAAAATGAAACGGG  
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTCT  
 CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA  
 TGCAATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCT  
 AGAAGGAAAAACAGATGCATGCCAGGGTGAECTGGAGGACACTGGTAGTTCAAGATGCTA  
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCAAACCCAACAAG  
 CCTGGTGTATAGAGTTACGGCCTTGGGGACTGGATTACTCAAAAACGGTATC**TA**  
**AG**AGACAAAAGCCTCATGGAACAGATAACATTTTTTGGTTGGGTGTGGAGGCCATT  
 TTTAGAGATAACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAC  
 TGTTGCTGATGCATGTATTCTTCCCTCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCAATTGTTCTCTAGAAGTTGTCAAGAATTGAC  
 TTGTTGACATAAATTGTAATGCATATATAACATTGAAGCACTCCTTCTTCAGTTCTC  
 AGCTCCTCTATTCAAGCAATATCCATTTCAGGTCAGAACAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAAATCCCCTACATTATTGGCACAGAAAAGTATTAGGTGTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCAATTGAAAGGTCAAGCAAAGACAGCAGAACATCAAC  
 ACTTCATCATTAGGAAGTATGGAACTAAGTTAAGGAAGTCCAGAAAGAACAGCAAGATATA  
 TCCTTATTTCATTCCAAACAACACTATGATAAAATGTGAAGAAGATTCTGTTTTGTG  
 ACCTATAATAATTACAAACCTCATGCAATGTAATTGTTCTAAGCAAATTAAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAAATAAAATAAATCACCCA

## **FIGURE 150**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVI FISLIVLAVCIGLT VHYVRYNQKKTNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLES MVKNAFYKSP LREEFVKSQVI KFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEW PWQASLQWDGSHRCGATLINATWL VSAAHCF TTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHP SHDYDISLAE LSSPV PYTNAVHRVCLPDAS YEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATT CNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDI WYLAGIVSWGDEC A KPNKPGVYTRVTALRDWITSKTGI
```

**Transmembrane domain:**

amino acids 21-40 (type II)

## FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATAACAACCTGACAGCA  
 CAGCCTGAGATCTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTCTGTGGCTCCTGGC  
 CGTGACCTTCTTGGTCCCAGAGCTCAGCCCTGGCCCTCAAGACTTGAAGAAGAGGAGG  
 CAGATGAGACTGAGACGGCGTGGCCGCCCTTGCCGGCTGTCCCCTGCGACTACGACCACTGC  
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTGGGCCGGCCTGCCTGTGCC  
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCATGGAGAAGTGCACATTGC  
 CCGAAGAGGGCCGCCAGTGGTCCACTGGTGTGCCCTCTCCCGTCCACTACTGG  
 CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCGCTGAACGCTACGGTCCG  
 CAGAGCCGAACTGAAGGGCTGAAGCCAGGGCATTATGTCGTTGCGTAGTGGCCGCTA  
 ACGAGGCCGGGGCAAGCCGCGTGCCCAAGGCTGGAGGAGAGGGCCTCGAGGGGCCGACATC  
 CCTGCCTTCGGGCCTTGCAGCCGCCTGCGGTGCCGCCAACCCCGCACTCTGGTCCACGC  
 GGCGTCGGGTGGCACGGCCCTGGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCACTTCT  
 GCCTGCGCAGTCGCTGGGCTGCCCGCCGAGCCGCCGAGCCGCAGGGCGCTC**TGA**  
 AAGGGGCCTGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTAGCCTGGCCCCCG  
 GGAAAGAGGAAAACCCGCTGCCCTCAGGGAGGGCTGGACGGCGAGCTGGAGGCCAGCCCCAG  
 GCTCCAGGGCCACGGCGGAGTCATGGTCTCAGGACTGAGCGCTGTTAGGTCCGGTACTT  
 GGCGCTTGTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGCCCCAATTTTTTTA  
 AGCGGCCAGATAATAATGTAACCTTGCAGGTTAAAAAAAAAAAAAAA

## **FIGURE 152**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCILLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAAACLCPGLSSPAQPPDPPRMGEVRIAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVHAAVGVTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

## FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCCGAAGAAGTTCC  
 CTGCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCAGGGCGTGGGCACCGGG  
 CCCAGCGCCGACATCGCTGCCGTTGCCCTGGGAGTAGGATGTGGTGAAGGATGGGC  
 TTCTCCCTACGGGCTACA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT  
 CTACGCCCTCAATCTGCTCTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTTGG  
 TGAGGGACTACCTAAATAATGTTCTCACTTAAC TGCAAGAACGAGGGTAGAGGAAGCAGTC  
 ATTTGACTTACTTCCTGTGGTCATCCGGTCATGATTGCTGTTGCTGTTCTTATCAT  
 TGTGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTGCATGGTACT  
 TTGGAAGTTGCTTGTCACTTCTGTAGAACTGGCTTGTGGCGTTGGACATATGAACAG  
 GAACTTATGGTCCAGTACAATGGTCAGATATGGTCAC TTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTCAGAGAGATTTAAGT  
 GCTGTGGAGTAGTATATTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCAGAT  
 TCCGTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA  
 CCTTATCAAGAGGGTGTGGGAAGAAAATGTATTCCCTTTGAGAGGAACCAAACAACTG  
 AGGTGCTGAGGTTCTGGGAATCTCCATTGGGTGACACAAATCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGCTCTGTATTATGATAGAAGGGAGCCTGGACAGACCAAATGATG  
 CTTGAAGAATGACAACCTCAGCACCTGTATGTCCTCAGTAGAACTGTTGAAACCAAGCC  
 TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAAATACACACTTGAGATGGAG  
 GAGTT**TAAA**AGAAATGTCACAGAAGAAAACCACAAACTGTTTATTGACTGTAATT  
 TTTGAGTACATACTATGTGTTCAAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTAAAATGAGGATGGAAAAGTTCATGTCATAAGTCAC  
 CACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCACTGCACTGTG  
 CTGTGTATGACTTTACTGAAACACAGTTATGTTGAGGCAGCATGGTTGATTGACATT  
 CGCATCCATGCAAACAGACTCACATATGGTGGACTGGAGCCATAGTAAAGGTTGATTACT  
 CTACCAACTAGTATATAAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTATTACTCAGCGATCTATTCTGTGCTAAATAATTATATCAGAAAACCTTC  
 AATATTGGTGAACACTAAATGTGATTGCTGGTTACTAAAATATTCTACCACTAAAA  
 GAGCAAGCTAACACATTGCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTGTTAAA  
 TCTGTATAATTCACTGATTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
 ATTGTCCGTATAGCATCATTATTTAGCCTTCTGTTAATAAAGCTTACTATTCTGT  
 CCTGGCTTATATTACACATATAACTGTTATTTAAACTTAACCACTAATTGAAAATTA  
 CCAGTGTGATACATAGGAATCATTATTCAAGAATGTTAGTCTGGTCTTAGGAAGTATTAATAA  
 GAAAATTGACATAACTTAGTTGATTCAAGAAAGGACTTGTATGCTGTTCTCCAAATG  
 AAGACTCTTTGACACTAACACTTTAAAAAGCTTATCTTGCCTCTCCAAACAAAGAA  
 GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATAAAACATGTGACAATTAGAGATTCTTGTGTTATTCACTGATTA  
 ATATACTGTGGCAAATTACACAGATTATTAAATTGTTACAAGAGTATAGTATATTATTT  
 GAAATGGAAAAGTGCATTTACTGTATTTGTGTTATTCTCAGAATATGGAA  
 AGAAAATTAAATGTGTCATAAAATATTCTAGAGAGTAA

## **FIGURE 154**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNVLTLTAETRVEEAVILTYFPV
VHPV рIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPQ
WSDMVTЛKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPГTDQMMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## FIGURE 155

GAGAGAGGCAGCAGCTGCTAGCGAACAGGATGCTGGCGTGAGGGACCAAGGCCTGCC  
 TGCACTCGGGCCTCCAGCCAGTGCCTGACCAAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTGGGGTACAATCTCAGCTCCAGGCTACAGGGAG  
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGTACAACCTCTGAACAGC  
 CTCGATGTCAAACCCCTGCGAAACCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
 CCCCACATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTGCCTCATCAAGG  
 TGATTCTGGATAAATACTACTTCCTCTGCAGGCTCTCCACTTCATCCGAGGAAGCAG  
 CTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
 CCCCAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
 ACTCGGCCACAGGAACTGGTCTGCCTGTTGACAACCTCACAGAACGCTCTCGCTGAG  
 ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA  
 TGGTGTGAAATCACAGAAAACAGCCAGGAGCTCGATCGGAACACTCAAGTGGCCCTGTC  
 TCTCAGGCTCCCTGGCTCCCTGCACTGTCTGCCTGTGGGAAGAGCCTGAAGACCCCCGT  
 GTGGTGGGTGGGGAGGAGGCCTCTGGATTCTGGCCTGGCAGGTCAGCATCCAGTACGA  
 CAAACAGCACGTCTGGAGGGAGCATTGGACCCCCACTGGTCCTCACGGCAGCCCAGT  
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGGCCAGGCTCAGACAAACTGGG  
 AGCTTCCCACCCCTGGCTGGCCAAGATCATCATCATTAATTCAACCCATGTACCCAA  
 AGACAATGACATGCCCTCATGAAGCTGCAGTCCCACACTTCTCAGGCACAGTCAGGC  
 CCATCTGTCTGCCCTTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGA  
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGCGTCAGTCCA  
 GGTCAATTGACAGCACACGGTCAATGCAGACGATGCGTACCAAGGGGAAGTCACCGAGAAGA  
 TGATGTGTGCAGGCATCCGGAAAGGGGTGTGGACACCTGCCAGGGTACAGTGGTGGGCC  
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGCATCGTTAGCTGGGCTATGGCTGCC  
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
 TCTGGAAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTGCACTGCTGGAGGCCCTGGTACACCC  
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGTACACCC  
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGCCCTCAATTCTGTAAGAGACCC  
 TCGCAGCCCAGAGGCCAGAGGAAGTCAGCAGCCCTAGCTGCCACACTGGTCTCCC  
 AGCATCCCAGGGAGAGACACAGCCCAGTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAA  
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTGGTAAAGGCCAGATCACTGTGG  
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGGCCCTGTCCTTCAACCCATCCCCAAGCCTA  
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
 ACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTATTAAAGAGCTGTAAACATCT  
 CTGGCAAAAAAA

## **FIGURE 156**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pi: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIVVVLIKVILDKYYF
LCGQPLHFI PRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAE TACRQMGYSRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGGEASVDSWPWQVSIQYDKQHVCGGSILDPHWLTAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDGGPLMYQSDQWHVVGIVSWGYZGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

**Transmembrane domain:**

amino acids 32-53 (typeII)

## FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGCATCCCCAGGCTCCAG  
 AGCTCCCTGGTACAGTCTGTGGCTGAGC**ATG**CCCTCCAGCCCTGGCCTGGACCCCTGGAGGCCTCCTGGGCC  
 TTTCCCTCTTCAACTGTTCACTGCTGCTGCCGACGACGCCGGGGAGGCAGGGCCATGCCA  
 GGGTCAGATACTATGCAGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCTCCAGGATTTGACA  
 CTCTGCTCTGAGTGGTATGGAAATACTCTACGTGGGGCTCGAGAACCCATTCTGGCTTGGATATCCAGG  
 ATCCAGGGTCCCCAGGCTAAAGAACATGATAACCGTGGCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTA  
 AGAAGAACAGCAATGAGACACAGTGTTCACACTCATCCGTGCTGGTTCTACAATGTCACCCATCTAC  
 CCTGCGGACACCTCGCCTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCCTACCTGTTGCCATCTCGG  
 AGGACAAGGTATGGAGGGAAAGGCCAAAGCCCCCTTGACCCGCTCACAAGCATAACGGCTGCTTGGTGGATG  
 GGATGCTCTATTCTGGTACTATGAACAACTCCTGGCAGTGAGCCATCCTGATGCGCACACTGGATCCCAGC  
 CTGTCCTCAAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCCTCTTGTCGGCAGGCCATCCCTCGACCC  
 AGGTCGCTACTTCTTCGAGGAGACAGCCAGCGAGTTGACTTCTTGAGAGGCTCCACACATCGGGGTGG  
 CTAGAGTCTGCAAGAACATGACGTGGCGGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTCCTGAAGGCCAGC  
 TGCTCTGCACCCAGCGGGGAGCTGCCCTCAACGTATCCGCCACGCCCTGCTCCCCGCCGATTCTCCA  
 CAGCTCCCCACATCTACGCAGTCTCACCTCCAGTGGCAGGTTGGCGGGACCAGGAGCTGCGGTTGTGCCT  
 TCTCTCTTGGACATTGAACGTCTTAAGGGAAATACAAAGAGTGAACAAAGAAACTTCACGCTGGACTA  
 CTTATAGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGCCCTCCTGATAAGGCCCTGACCT  
 TCATGAAGGACCATTCCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTAAATCTGGCGTGGAGTATA  
 CACGGCTTGAGTGGAGACAGCCAGGGCCTTGATGGCACAGCCATCTTGTATGTACCTGGAACACCACAG  
 GGTCGCTCCACAAGGCTGTTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTGAGCTGTTCCCTGACC  
 CTGAACCTGTTGCAACCTGCACTGGCCCCCAGGGTGCAGTGTTGAGGCTCTCAGGAGGTGCTGGA  
 GGGTGGCCCGAGCCAACGTAGTGTCTATGAGAGCTGTTGAGCTGTCCTGGCCGGGACCCCCACTGTGCCT  
 GGGACCCCTGAGTCCGAAACCTGTTGCCCTGTCTGCCCTAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG  
 GGAACCCAGAGTGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTCGGCCTCAGAGCCGGCGAAATCATTA  
 AAGAAGTCCTGGCTGTCCCCAACTCCATCTGGAGCTCCCTGCCCTACCTGTCACTGGCTGGCTTATTATT  
 GGAGTCATGGCCCAAGCAGCAGTCCAGAAGCCTCTTCACTGTCTACAATGGCTCCCTTGTGATAGTCAGG  
 ATGGAGTTGGGGTCTCTACCAAGTGTGGCAACTGAGAATGGTTTCACTACCCGTGATCTCCTACTGGTGG  
 ACAGCCAGGACCAGACCCCTGGCCCTGGATCTGAACGTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCGTTGA  
 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCACTTGTCACTGTCAGTGCCT  
 TTGCCCTAGTGTCTCAGGAGCCCTCATCTCGTGGCTCCCAATTGAGAGCACTCCGGCTCGGGCAAGG  
 TTCAGGGCTGTGAGACCCCTGCCCTGGGGAGAAGGCCCTGTTAAGCAGAGAGCAACACCTCAGTCTCCAAAGG  
 AATGCAGGACCTCTGCCAGTGTGGACGCTGACAACAACTGCCTAGGCAGTGGTAGCT**TAA**ACTCTAGGCA  
 CAGGCCGGGCTCGGGCAGGCACCTGCCATGCTGGCTGGCGGCCAAGCAGCAGCCCTGACTAGGATGACAG  
 CAGCACAAAAGACCACCTTCTCCCTGAGAGGAGCTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG  
 ATGCACAGCAGTCTGCCCTCCCTATGGACTCCCTTACCAAGCAGCATGAGCTCTCAACAGGGTGGGGCTAC  
 CCCCAGACCTGCTCTACTGATATTGAAGAACCTGGAGAGGATCCTCAGTTCTGGCATTCCAGGGACCCCTC  
 CAGAACACAGTGTTCAGAGACCCAAAAACCTGCCCTGCTGGCTCCAGGACCCATGGTAATGAACACCAAACATC  
 TAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGTTGGACACCAACACTCC  
 TCTCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAAGTGTGACCGCTGACTCCAGGAAGTC  
 TTTCCCTGAAGTCTGACCACTTCTTGTGCTTCAAGTGGGGCAGACTCTGATCCCTCTGCCCTGGCAGAATGG  
 CAGGGGTAATCTGAGCCTCTTACCTTACCCTAGCTGACCCCTCACCTCTCCCCCTCCCTTCTTGT  
 TTTGGGATTCAAGAAAATGCTGTCAGAGACTGTTATTTTATTAAACATATAAGGCTTAAAAAA

**FIGURE 158**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLPTTAGGGGQGPMPPRYYAGDERRALSFFHQKGLQ
DFDTLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVFVFF
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTOGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

```

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704

## FIGURE 159

AGGGTCCCTAGCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGGCTTCCGTAGAAG  
 TGAGC**ATGG**CTGGGCAGCGAGTGCTTCTTAGTGGCTTCTCCCTGGGTCTGCTC  
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTAACCAACAAAAGAG  
 GTCCTTTATGCCAGATTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTCTTCTGGAAGAAACTTCTAGG  
 TGGCAGAGGAAAATTGAAAACTTATAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
 ATTTTTAAATAGAAAGGATATCATGGATTCCCTAAAGAATGAGAACACTCGACATGGTGATA  
 GTTGAACACTTTGACTACTGTCCTTCTGATTGCTGAGAAGCTGGGAAGCCATTGTGGC  
 CATTCTTCACTTCATTGGCTCTTGGAAATTGGGCTACCAATCCCCTGTCTTATGTTC  
 CAGTATTCCGTTCTGCTGACTGATCACATGGACTCTGGGGCCGAGTGAAGAATTCTG  
 ATGTTCTTAGTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTGACAACACCATCAA  
 GGAAACATTTCACAGAAGGCTCTAGGCCAGTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTCACTTAACACTGACTTGCCTTGATTGCTGACCTCTGCTTCCAAACACTGTTAT  
 GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCAAGACTTGGAGAACTTCATTGC  
 CAAGTTGGGACTCTGGTTGTGACCTTGGCTCATGGTGAACACCTGTCA  
 ATCCGAAATCTCAAGGAGATGAACAATGCCTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTAGTGTCTCATTGCCCAAAGATGTCACCTGGCTGCAAATGTGAAAATTGTGGA  
 CTGGCTCCTCAGAGTGCACCTCCTGGCTCACCAAGCATCCGTCTGTTGTCACCCACGGCG  
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCTTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTGGTGTCTATTGAGT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGGCGAGTGGCTGCCAGTGTCTGCACCTCCCACCGCTCAGCCCCACACAG  
 CGGCTGGTGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCAGCACCTCAAGCCCTA  
 TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCGACGTTTGTGTTCTGCTGGGGC  
 TCACTCTGGGACTCTATGGCTTGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**AGGCCAGGTGCAAGCCTGGCGGGCTGTTGGTGG  
 GCGATGTCACCATTCTAGGGAGCTTCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTC  
 TAGTTATCTCCTGTTCTGAAGAACAGGAAAAATGCCAAAATCATCCTTCCACTTG  
 TAATTTGCTACAAATTCTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT  
 CTTGTCCTCTTGTGCTGCCATCAGCAAGGGCTATGCTGATTCTGTCTGAGTGACTTG  
 GACCACTGACCCTCAGATTCCAGCCTAAACACCTCCCTCATGCGCCTCTCCGAA  
 TCACACCCCTGACTCTCCAGCCTCCATGTCAGACCTAGTCAGCCTCTCATCCTGCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTCTTCAGTTCTGTT  
 TGTTCTCCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCA  
 CGGACACAGGCTCACAGGTCTCCACATTGGTCCCTGTCTGGTGCACAGTGAGCTCCT  
 TCTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCTGAAAAATAAAAGTTACA  
 GCGTTATCTCCCCAACCTCACTAA

## **FIGURE 160**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pi: 8.68, NX(S/T): 1
MAGQRVLLLGVFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIDMSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFARPLLPTVYVGGIMEKPIKPVQPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVKLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPLFQDQOPENMVRVEAKKFGVSIQLKKLAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVVFLLGLT
LGTLWLCGKLLGMAVWWLRGARKVKET
```

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

## FIGURE 161

GGGCTGTTGATTGTGGGGATTTGAAGAGAGGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTCTGTCACACCCGTACACACACATACCATGTT  
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCTCATCCAGCAGGGCTACCCCTGAAGCTCT  
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTCATCCCTCCTTCTCTCCCAAAGCCCA  
 ACTGCTGTCACTGCATGCTGCCAAGGAGGAGGAACTGCAGTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGTTCAGCGAGCCTAGAGAGGGC  
 AGACTATCAGGGTGCCGGCGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGAGA  
 AGACCGGGCACTTGTGGGTTGCAGAGCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGC  
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTGGTTCTGGTGCTTCTGGCCCTGGGGC  
 GGGTGGGCCAGGAGGGTCAGAGCCGTCTGCTGGAGGGGAGTGCCTGGTGGTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGC  
 GAGTGGCATTGCTGCGGTCCGAAGCCACCACATGAGCCAGCAGGGAAACCGGCAATGGC  
 ACCAGTGGGCCATCTACTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTGACCGGGC  
 CTCTGGCTCTCGTAGCCCTGTCCGGGTGCTACAGCTCCGGTTCCATGTGGTGAAGG  
 TGTACAACCGCAAACACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCTGTCACTCAGCC  
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACAGCTCTGTGCTACTGCCCTTGG  
 CCCTGGGACCGAGTGTCTGCGCCTGCGTCGGGAAATCTACTGGTGGTGGAAATACT  
 CAAGTTCTGGCTTCCATCTTCCCTCT**TGA**GGACCAAGTCTTCAAGCACAAGAAT  
 CCAGCCCCTGACAACCTTCTGCCCCCTCTTGGCCAGAAACAGCAGAGGCAGGGAGAG  
 ACTCCCTCTGGCTCTATCCCACCTCTTGATGGACCCCTGTGCCAAACACCCAAAGTTAA  
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTCCACCCACCCACCCAGTTACC  
 CTCCCAGCCACCTGCTGCATCTGTTCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA  
 AGAAGGAAGATCTGCACTACTTGCAGGCTCTGCTCCTCCGGTCCCCACCCAGCTTCC  
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCAG  
 ATGGACAAGCCTCAGCGTACCCCTGCAGGCTTCTCCTGTGAGGAAAGCCAGCATCAGGATC  
 TCAGCCAGCACCCTGCAAGCTGAGCCAGCACCGTATGGCTAGGGTGGAGGCTCAGCCAC  
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTAGGAAGGAAGGAGGGTGTATTG  
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
 GGCTGTCCTCTATGCTGGATCCCAGATGGACTCTGCCCTTACCTCCCCACCTGAGATTAG  
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAAAACATCGATAACCAGCATCCTTGTGGCCACCTCCTGAAACTGCTCCAC  
 CTTGAAAGTTGAACTTCTAGTCCCTCCACACTCTGACTGCTGCCCTCCTCCCAGCTCTC  
 TCACTGAGTTATCTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTTCTCTGAT  
 CTGTGCTGCTTATTCTCCTCTTAGGCTTCTATTACCTGGGATTCCATGATTCAATTCT  
 CAGACCCCTCCTGCCAGTATGCTAAACCCCTCCCTCTCTTTCTTATCCCGCTGTCCCCATT  
 GGCCCAGCCTGGATGAATCTATCAATAAAACAACAGAGAATGGTGGTCAGTGAGACACTAT  
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA  
 TGTGCAAGAGAAAATAATCAAACGTATACTAAAATTAAAAA

## **FIGURE 162**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFAANDPDVTREAATSSVLLPLDPGDRVSIRLRRG
NLLGGWKYSSFSGFLIFPL
```

**Signal peptide:**

amino acids 1-32

## **FIGURE 163**

GCTTTCTCGGCCACCACTGGCCGCCGGCGCAGCTCCAGGTGTCCTAGCCGCCAGC  
 CTCGACGCCGTCCGGGACCCCTGTGCTCTGCGCAAGCCCTGGCCCCGGGGCCGGGCAT  
 GGGCCAGGGCGCGGGGTGAAGCGGCTCCCGGGGCGGTGACTGGCAGGCTCAGGCC**AT**  
**GAAGACCCCTCATGCCCTACTCCGGGTCTCGCGCGAGCGTCAGGCCGAGGCTGACC**  
 GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGCGCGAGGGCTGGGAGATGGGCACT  
 GGATCCAGCATTCTCCGCCCTCCAGGACCTCTCTGTCACCTGGCTCAATAGGTCAA  
 GGTGGAAAAGCAGCTACAGGTATCTCAGTGCTCCAGTGGCTCTGCTCCTGTACTGG  
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTATCGCTGTG  
 CTCTACTTCACTGGCTGGTGTGACTGGAACACACCAAGAAAGGTGGCAGGAGGTACACA  
 GTGGGTCCGAAACTGGGCTGTGCGCTACTTCGAGACTACTTCCCATCCAGCTGGTGA  
 AGACACACAAACCTGCTGACCACCAGGAACATATCTTGGATACCACCCCCATGGTATCATG  
 GCCCTGGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTCCCAGG  
 CATAACGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCGTGAGGGAGTACC  
 TGATGTCTGGAGGTATCTGCCCTGTCAAGCCGGACACCATAAGACTATTGCTTCAAAGAAT  
 GGGAGTGGCAATGCTATCATCATCGTGGTCGGGCTGAGTCTGAGCTCCATGCC  
 TGGCAAGAATGCAGTCACCTCGGAACCGCAAGGGCTTGTGAAACTGGCCCTGCGTCATG  
 GAGCTGACCTGGTCCCCTACTCCTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTC  
 GAGGAGGGCTCCTGGGCCATGGTCCAGAAGAAGTCCAGAAATACATTGGTTGCC  
 ATGCATCTCCATGGTCGAGGCCTTTCTCCGACACCTGGGGCTGGTGCCTACTCCA  
 AGCCCATCACCACGTGGAGAGGCCATCACCATCCCCAAGCTGGAGCACCCAACCCAG  
 CAAGACATCGACCTGTACCAACCATGTACATGGAGGCCCTGGTGAAGCTTCGACAAGCA  
 CAAGACCAAGTCGGCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTCGGG  
 GCCAATTCCCTGGAGGAACCAAGCTGCAAATCACTTTGCTCTGAAATTGGAAAGTGTCA  
 TGGGTGTCTGTGGTTATTAAAAGAAATTATAACAATTGCTAAACCAAAAAAAA  
 AAAAAAAA  
 AAAAAAAA

## **FIGURE 164**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMGGICPVSRTDIDYLLSKNGSGNAIIVVGGAAESLSSM
PGKNAVTLRNRKGKVKLALRHGADLVPYIYSGENEVYKQVIFEEGSWRVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPIТИPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

## FIGURE 165

GGGCGGGCGGGATGGGGGCCGGGGCGGGCGCCGACTCGCTGAGGCCCGACGCAGGGCCGGCCGGCCCA  
 GGGCGAGGAGCGCGGCGGCCAGAGCAGGGCGAGGCAGGCCGGGACGCCGCGCAGCAGCAGGTGGCG  
 GCGGCTGCAGGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCACTGGCTCTGCTGACCTTGTGCCTTGA  
 CGGCTGTCTCAGCGAGGGCCGTGCACCCGCTCTGAGCAGCGC**TGA**GGCCTGCTGGCCTCCTGAAGACCCA  
 GTTCGTGCTGCACCTGCTGGTGGCTTGTCTCGTGGTGAAGTGGTCTGGTATCAACTTGTCCAGCTGTGCAC  
 GCTGGCGCTGGCCGGTCAGCAAGCAGCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA  
 ACTGGTCATGCTGCTGGAGTGGTGGCTGACGGAGTGTACACTGTTACGGACCAGGCCACGGTAGAGCGCTT  
 TGGGAAGGAGCACGCAGTCATCATCTAACCAACTTCGAGATCGACTCCCTGTGGGTGGACCATGTGTGA  
 GCGCTTCGGAGTGTGGGGAGCTCCAAGGTCTCGTAAGAAGGAGCTGTCTACGTGCCCTCATCGGCTGGAC  
 GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG  
 GCGCCTGTCGGACTACCCCGAGTACATGTGGTTCTCCTGTACTCGAGGGGACCGCGCTCACGGAGACCAAGCA  
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAACGGGCTTCTGCTCAAGTACCACTGCTGCCGCGGACCAAGGG  
 CTTCACCAACCGCAGTCAAGTGCCTCCGGGGACAGTCGAGCTGTATGATGTAACCTGAACCTCAGAGGAAA  
 CAAGAACCGTCCCTGCTGGGATCCTCTACGGAAGAAGTACGAGGGGACATGTGCGTGAAGGAGATTTCTCT  
 GGAAGACATCCCCTGGATGAAAAGGAAGCAGCTCAGTGGCTTACAAACTGTACCAAGGAGAAGGACCGCCTCCA  
 GGAGATATATAATCAGAACGGCATGTTCCAGGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCCTGAA  
 CTTCCGTGCTGGGCCACCATTCTCTGTCTCCCCTCTCAGTTGTCTGGCGTCTTGCCAGCGGATCACC  
 TCTCCTGATCCTGACTTTCTGGGTTGTGGAGCAGCTCCTTGGAGTTCGCAGACTGATAGGAGAATCGCT  
 TGAACCTGGGAGGTGGAGATTG**CAGTGA**GCTGAGATGGCATCACTGTAAGTCCAGCCTAGGAAACAGAGCAAGACT  
 CAGTCTAAAAAAAAACAAAAACCCAGAAATTCTGGAGTTGAACCTGTAGTTACTGACATGAAAA  
 ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGGCAGAAAAAAATCAGCAAGCTGAAGATGGTACCTGAGATT  
 TTTCAGGCTAATGAAAAAGAATGAAGGAAAATTACAGCCTCAGAGACCCATGGTCACCGTCACACAAATCAA  
 CATATGCATGATGAGAGTCCCAGAACGGAGAGGAGAACGGGTCAGAAAGAATGCCACAAGCTGATGAAAAACA  
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT  
 AATCAAAGTGTCAAATGACAAAGAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTGTTCAAAGGATCTTG  
 ATCAGATTAACAGCTCATTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA  
 AACCTCAACTGTAATTATTGGACTTTGAGTCTTAGATGGCCTGACCTCTTGTCTCAGGGACAGTTTCA  
 ATTAAATCCCTAATAACAATTAGTCAGGCTTCCCTGACCTGTAGGAAGGCCGTCTTAGGCCGGACAGTGGC  
 TTACACCTGTAATCCCAGCATTGGGAGGCCAGACGGTGGATCATTTGGGTCAGGCTGATCTCAAACCTCT  
 GAGTTCAGGTGATCTGCCGCTCAGCCTCCAAAGTGTGATTGCAGGCGTGAAGCCACTGCGCCTGGCGGA  
 ATTCTTTTAAGGCTGAATGATGGGGCCAGGCACATGGCTCACGCCGTGATCCCAAGTAGCTTGATTGTA  
 AACATGCACCAACATGCCTGGCTAATTGTTAGAGACAGTGTAGCCAGGCTGGTCTCGATCTCCT  
 GACCTCAAGTGAACCTGCCTCAGCCTCCAAAGTACTGGGATTACAGGCGTGAAGCCACTGTCCTGCCCTGA  
 GCATCTGTGATGTGCTTATTGCCATTGTATATCTTCTATCTTCTTGGGAAATGTCTGTTCAAGTCCTTG  
 CCTTTTAAATTATTATTATTATTATTATTGAGACAGGGCTTGTCTGTTGCCAGGCTGGAGTA  
 CAGTGGCACAGTCTGGCTCACTGCAGCCTCGACCTCCTGGCTGAGTGTACCTCCACCTCAGCCTCCCTGT  
 AGCTGTATTGTTGTATTGTTGAGCTGTAGTTGTATTGTTGTGGAGACAGCATTTCACCATGA  
 TGGCCAGGCTGGCTTGAACCTGAGCTCAAGTGTACCTGCTTCAAGCCTCCAAAGTGTGGGATTACAGA  
 CATGAGCCACTGCACCTGGCAAACCTCCAAATCAACACACACACACACACACACCTGATTCAAATGGGCA  
 GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTGGCATGAGAAGTCGAGGCTG  
 CAGTGAAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAAACAGAGTGAAGACCCTGTCTC

## **FIGURE 166**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pi: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFIEDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPIDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPFSFVLGVFASGSPLLIITFLGFVGAASFGVRRILIGESLEPGRWRLQ
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

## FIGURE 167

GATATTCTTATTTAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA  
 GCCACCAGGCATATTCATCTTGTGTGTTTCTTTGCTTAGCACTGGGGCACTTCTT  
 GCTTATTCTTGGTAGGAAAGGGGCTCAGTTGTCTTGGGGTGGCAGGCAGGCCG  
 GCTTACGCCTGATAACGCCCTGGGTTAGAAGGGAAGGAAAGATAAACTTTATACAAATGGG  
 GATAGCTGGGTCTGAGACCTGCTCCTCAGTAAAATTCTGGATCTGCCTATACCTTCTT  
 TTCTCTAACCTGGCATACCCTGCTAAAGCCTCTCAGGGCTCTCTGTTCTAGGATCAA  
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTCATTGT  
 ACATGTGGTGTCTTGTGTTCTG**TAA**TGTGGTATGCCATGGGTCTTGCACAAGCCT  
 TTCCTTTGGCTGGACACTGTTCCCTGCCCCCCCCACTCTTCTACTTAATATGTAGTC  
 ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
 CTTGTTAATGCTCTCATAGACCACTGTTCCCTTGCAGCACTGCCACTCAGTTGTA  
 TCTTATGTGCGTTGTGGTTGTATGGTTGTCTGTTCCCTGAGCAGTACATGTGGTGGTGCT  
 TGCAGGGTCAAGGCATTGCTGTGCCTGCCAGGTATAGTCCTACATGTGGTGGTGCT  
 CATGTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAGATTGAAATCTCTCAGTTACCA  
 GATGGTGTAGGGCCCAGCATTGTAATTACACGTTGACTGTGCTTGTGAATTATCTGGGGAA  
 TGCAGGTCTGATTCACTAGGCCAGGTTGGCATCTCTAACAAACTCCCACGTGATGCTGA  
 TGCTGGTCCTATGAACTATAACTAAATAGTAAGAATCTATGGAGCCAGGCTGGCATGGTGGC  
 TCACACCTATGATCCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCATCTGACTAAAAATACACAAATTAGCTG  
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGA  
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

## **FIGURE 168**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWVRR
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

## FIGURE 169

GGCTGGACTGGAACTCCTGGTCCCAGTGATCCACCCGCCCTCAGCCTCCCAAGGTGCTGTGA  
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTCAAGCAACTAAAAAGCCAC  
 AGGAGTTGAAC TGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
 ATTAAAATCTGTTTTGTTCTTGTAAC TAGCCTTACCTCCTAACACAGAGGATCTGT  
 CACTGTGGCTCTGGCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCAC  
 ACCGTCCTCGAAGCCGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
 ACCAACTGTCTCACGTCTGGAGGACTGACTCGGGCAGTCAGGTAGCTGAGCCTTGGTA  
 GCTGCGGCTTCAAGGTGGGCTTGCCCTGGCGTAGAAGGGAT**TGA**CAAGCCGAAGATT  
 CATAGGCGATGGCTCCACTGCCAGGCATGCCCTGCTGTAGTCATCAACTGCCCTGGGG  
 CCAGGACGGGCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCGCCAT  
 CTAACCTTTCATGTCCTGCACATCACCTGATCCATGGCTAATCTGAACCTGTCCCAAGG  
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGTCTGCTTAGACCACCTGGTT  
 TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
 GGGAAAGGAACTTGTGCCAAATTATGGGTCAAGAAAAGATGGAGGTGTTGGTTATCACAAGGC  
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTGCCATGGCGCATGACACACT  
 CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACCAAGCTGCTG  
 AAGGGCAACTGCAGGCCATGCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACCAG  
 CCAGGGGCAGCGTCTGGAAAGGAGCAAGCAAAGTGACCAATTCTCCTCCCTCCTCCCTC  
 TGAGAGGCCCTCTATGTCCTACTAAAGCCACAGCAAGACATAGCTGACAGGGCTAATG  
 GCTCAGTGTGGCCAGGAGGTCAAGCAAGGCCTGAGAGCTGATCAGAAGGGCTGCTGTGCG  
 AACACGGAAATGCCCTCAGTAAGCACAGGCTGAAAATCCCCAGGCAAAGGACTGTGTGGCT  
 CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTGTATTGAAATTGAAACCCAAA  
 TCCAAACCTAAGAACCCAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTTGGCCTGTAATG  
 CCAACATTGGGAGGCCAGGCGAGGCGGGTAGATCACCTGAGGTCAAGGAGCTGACAGGACTGCTG  
 GCCAACATGGTGAACCCCTGCTCTACTAAAAATACAAAAAAACTAGCCAGGCATGGTGGT  
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTGAAACCTGGGAGGT  
 GAAGGAGGCTGAGACAGGAGAATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
 AAAAATAAAAAAGAATTATGGTTATTGTAA

## **FIGURE 170**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD
```

**Signal peptide:**

amino acids 1-15

**FIGURE 171**

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCAGTCCTGCCTC  
CCGCCGCCTCCTGCCCGCGCC**ATG**ACCCAGCCGGTGCCCGGCTCTCCGTGCCCGCGCT  
GGCCCTGGGCTCAGCCGACTGGCGCCGCCCTCGCCACTGGCCTCTTCCCTGGGGAGGGCGGT  
GCCCCCCATGGCGAGGCCGGCGAGAGCAGTCGCTGCTTCCCCCGAGGACAGCCGCTGTGG  
CAGTATCTTCTGAGCCGCTCCATGCAGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
CCTGGAGCAGCCGCAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTTGGCCAACC  
TGGCGCGGCTCATCCAGGCCAAGAAGGGCGTGGACCTGGCACCTCACGGCTACTCCGCC  
CTGGCCCTGGCCCTGGCGCTGCCCGGGACGGCGCGTGGTACCTGCGAGGTGGACGCGCA  
GCCCGGGAGCTGGGACGGCCCTGTGGAGGCAGGCCGAGGCCGAGCACAAAGATCGACCTCC  
GGCTGAAGCCCCTGGAGACCCCTGGACGAGCTGCTGGCGCGGGCGAGGCCGGCACCTTC  
GACGTGGCCGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
GCTGCTGCGACCCGGAGGCATCCTGCCGTCTCAGAGTCCTGTGGCGCGGAAGGTGCTGC  
AACCTCCGAAAGGGGACGTGGCGCCGAGTGTGCGAAACCTAACGAACGCATCCGGCGG  
GACGTAGGGTCTACATCAGCCTCTGCCCTGGCGATGGACTCACCTGGCCTCAAGAT  
**CTA**GGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTGCCTGGAACCCAGGAATTGAC  
CTGAGTTTAAATTGAAAATAAAGTGGGCTGGGACACAAAAAAA

## **FIGURE 172**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pi: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDLLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

## FIGURE 173

CCGCCGCCGCAGCCGCTACCGCCGCTGCAGCCGCTTCCGGCCTGGGCCTCTGCCGTCA  
 GC**ATG**CCACACGCCTCAAGCCCAGGGACTTGGTGTGCTAAGATGAAGGGCTACCCCTCAC  
 TGGCCTGCCAGGATCGACGACATCGCGATGGCGCCGTGAAGCCCCACCCAAACAAGTACCC  
 CATCTTTCTTGGCACACAGAAACAGCCTCCTGGGACCCAAGGACCTGTTCCCTACG  
 ACAAATGTAAAGACAAGTACGGGAAGGCCAACAAAGAGGAAAGGCTCAATGAAGGGCTGTGG  
 GAGATCCAGAACAAACCCCCACGCCAGCTACAGCGCCCCCTCCGCCAGTGAGCTCCTCGACAG  
 CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACATGAGGACCGGG  
 GGGTCATGGCGTCACAGCGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA  
 GACTCAGAACAGAGTAGCGACAAACAGTGGCCTGAAGAGGAAGACGCCCTGCCTAAAGATGTC  
 GGTCTCGAACAGAGCCGAAAGGCCCTCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG  
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCGAGCGACCAGGACTTCACACCT  
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAAAGAA  
 GGCGCGTCAGCCTCCGACTCCGACTCCAAGGCCGATTGGACGGGCCAGCCTGAGCCGG  
 TGGCCATGGCGCGTCGGCGTCCTCCTCCCTCTCTCTCTCCCTCCGACTCCGATGTG  
 TCTGTGAAGAAGCCTCCGAGGGGAGGAAGCCAGCGGAGAAGCCTCTCCGAAGCCCGAGG  
 GCAGAACCGGAAGCCTGAACGCCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG  
 TGGACCGCATCAGTGAGTGGAGCGGGGACGAGGCGCGAGGCGCAGCTGGAGGCCCG  
 CGCGCGAGAGCAGGAGGAGCTCGGGCGCTCGGGAGCAGGAGAAGGAGGAGAAGGA  
 GCAGGAGGCGCAGCAGGGCGACCGCGGGGAGGCTGAGCGGGGCAGCGCGGCAGCAGCGGG  
 ACGAGCTCAGGGAGGAGCAGTGAGCCCCTGAAGAACGCGGGAGCAGCAAGGCCGGGCCGG  
 CCCCCGTCTCCTCTGACTCCGAGCCGAGGCCAGCTGGAGAGAGAGGCCAAGAAATCAGC  
 GAAGAACGCCAGTCCTCAAGCACAGAGCCGCCAGGAACCTGCCAGAAGGAGAAGAGAG  
 TGCGGCCGAGGAGAACAAAGCCAAGCCCCTGAAGGTGGAGCGGGACCCGGAAGCGGTCC  
 GAGGGCTTCGATGGACAGGAAGGTAGAGAACAGAACAGGCCCTCCGTGGAGGAGAAGCT  
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTCGACAGCCGGACGTGAAGAGGT  
 GCCTGAATGCCCTAGAGGAGCTGGGAACCCCTGCAGGTGACCTCTCAGATCCTCCAGAAC  
 ACAGACGTGGTGGCACCTTGAAGAACAGATTGCCGTTACAAAGCGAACAGGACGTAATGGA  
 GAAGGCAGCAGAACAGTCTATACCCGCTCAAGTCGGGTCTCGGCCAAAGATCGAGGCGG  
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAACGGAGAACGCCGAGGAGAACGCTGGCCGG  
 GAGCTGGCCGGGAGGAGGCCAGGAGAACGCCAGGAGAACGCCAGCACCGATCTCTC  
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAACGGGAGAGCGCAGAGAACAGGAGCACG  
 AGGAGGGTGGGACTCGGAGGAGGGCCAAGGTGTGGCTCTGAAGACCTGCACGACAGC  
 GTACGGGAGGGTCCCGACCTGGACAGGCCTGGAGCGACCGGGCAGGAGCGAGAGGGCAGC  
 GGGGGACTCGGAGGCCCTGGACAGGAGAGCT**TGA**GCCGCCGGCAGCCAGGCCAGCCCC  
 CCGAGCTCAGGCTGCCCTCTCCTCCCCGGCTCGAGGAGAGCAGAGCAGAGAACGTGGG  
 GAACGCTGTGCTGTTGATTGTTCCCTGGGTTTTTCTGCCTAATTCTGTGATT  
 TCCAACCAACATGAAATGACTATAAACGGTTTTAATGA

## **FIGURE 174**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNNKYPPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGKPNKRKGFGNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDEDRG
VMAVTAVTATAASDRMESDSDDKSSDNSGLKRKTPALKMSVSKRARKASSLDQASVSPSE
EENSESSSESEKTSQDFTPEKKAAVRAPRRGPLGGRKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDDVSVKKPPRGRKPAEKPLPKPRGRKPAPPERPPSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAEEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEEKLAGELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGEESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES
```

**Signal peptide:**

amino acids 1-13

## FIGURE 175

GTGGGTTCTGGATCTCACCTTACCAACTGCAGATCTGGGACTCATCAGCCTCAATAATTATATTAAATTA  
 ACACCATTGAAAGAGAACATTGTTTCATC**ATG**AATGCTAATAAGATGAAAGACTTAAAGCCAGAAGCCAAGA  
 TTTCACCTTTCTGCTTGATGATGCTAACGATGACATGACATGTTCTTCAGTCAGTCAGTCAGTCAGTCAG  
 AAATATTCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTCAAAATAGCTGTATTCCCTTTGGGTTCATC  
 AGAAGGACTGGATTTCAAACCTCTCTTAGATGAGGAAGAGGCAAGGCTGCTCTGGAGCCAAGACCACAT  
 CTTCTACTCAGTCTGGTGACTTAAACAAAATTAAAGAAGATTATTGGCTGCTGCAAAGGAACGGGTGGA  
 ATTATGTAATTAGCTGGAAAGATGCCAACAGAATGTGCAAATTCTAGAGTACTCAGCCCTATAACAA  
 AACTCACATATATGTGTGGAACGGAGCATTCTAACATGAGGTTATGGAGTCTGGCAGACTGAAATGCTACAGGA  
 GGATATTATATTCAAACACTAGACACACATAATTGGAGTCTGGCAGACTGAAATGCTCTGGATCCTCAGCAGCC  
 TTTGCTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTCTGATTCCCTGGCAAAGATACTGCATT  
 CACTCGATCCCTGGGCCTACTCATGACCACACTACAGAACTGACATTTCAGAGCACTACTGGCTCAATGG  
 AGCAAAATTATTGAAACTTCTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTCG  
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACATCCTTCTGAGTTGGAAGAGTTGTAAGAATGATGT  
 AGGAGGACAACGCGCCTGATAAACAAAGTGGACGACTTCTTAAGGCCAGACTGATTGCTCAATTCTGGAAAG  
 TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTATTAACCCCCACAAGAGATGAAAGAAATCCTGT  
 AGTATATGGAGTCTTACTACAACCAGCTCCATCTCAAAGGCTGCTGTTGTGTATAGCATGGCTGACAT  
 CAGAGCAGTTTAATGGCCATATGCTCATAAGGAAGTGCAGACCATCGTTGGGTGAGTATGATGGGAGAAT  
 TCCTTATCCACGGCTGGTACATGCTCAAGAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTCAGA  
 TGATGTCATCAGTTCTAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTCGAGGAGGACCAACGTT  
 CAAGAGAATCAATGGAATTACAGACTGACACAGATAGTGGTGGATCATGTCATTGAGAAGATGGCCAGTACGA  
 TGTAATGTTCTGGAAACAGACATTGGAACTGCTCTCAAAGTTGTCAGCATTGAGTCTTCAAAGGAAAAGTGGAAATATGGA  
 AGAGGTAGTGTGGAGGGATTGAGTATTCAAGCACTCATCAATCATCTTGACAGATGGAATTGTCAGCAG  
 GCAACAATTGTACATTGGTCCCGAGATGGATTAGTCAGCTCCTTGACAGATGCGACACTATGGGAAAGC  
 TTGCGCAGACTGTTGTCTGCCAGAGACCCCTACTGTCCTGGATGGAATGATGTCATGCTCGATATGCTCCTAC  
 TTCTAAAAGGAGAGCTAGGCCAACATGTAAAATATGGCAGCCAAATCACCCAGTGTGGACATCGAAGACAG  
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTGGCATTGAAATTAACTCAACCTTCTGGAATGTATACC  
 TAAATCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGATGAGCATCGAGAGGAGTTGAGGCA  
 TGAAAGAATCATCAAACCGAATATGGCTACTGATTGAGTGTGAGAAGAAGGATTCTGGATGTTACTG  
 CAAAGCCCAGGAGCACACTTCATCCACACCATAGTGAAGCTGACTTGAATGTCATTGAGAATGAAACAGATGGA  
 AAATACCCAGAGGGCAGACATGAGGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGTTGAGATACAAAGA  
 CTACATCCAATCCTTAGCAGCCAAACTCAGCCTCGACCAGTACTGCAACAGATGTGGCACAGGGAGAAGCG  
 GAGACAGAGAAACAAGGGGGCCAAAGTGGAAAGCACATGAGGAATGAGAAGAAACGAAATCGAAGACATCA  
 CAGAGACCTGGATGAGCTCCCTAGAGCTGAGCCACG**TAG**TTTCTACTTAATTAAAGAAAAGAATTCTTAC  
 TATAAAAACATTGCTTCTGTTTGATATCCCTATAGTAATTCTAAATGCTCCATGGAGTTGCTAAGG  
 CACAAGACAATACTGAAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCTGAACCAGTTT  
 CCAAGAACAAATCTGACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGTTACAGTTGTAATGTTTAA  
 TGTTTGAGTTGGAATTATTGTCATGTAATAGTTGAGCTAAGCAAGCCCGAATTGATAGTGTATAAGGT  
 GCTTCTATTCCCTCGAATGTCATTAAGCATGGAATTACCATGCAAGTTGCTATGTTCTATGAACAGATATAT  
 CATTCTATTGAGAACCCAGCTACCTTGCTGAGGGATAAGAGGTGAGACACAAATTAGACAACCTCCATTATC  
 AACAGGAACCTCTCAGTGGAGCATCCTCTGGAGAATGGTATAGGAATTGGAGGGTGCATTATTCTTCT  
 TGGCCACTGGGTTAAATTAGTGTACTAACACATTGATTACTGAAGGGCAACTATGTTCCCCAGGAGTTCT  
 ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGTAGTTAGTGTGTTTAGAGTATATACTAA  
 GCTCTACAGGGACAGAATGTTAATAAAACTTTAATAAGATATGGAAAATTCTTAATAAAACAAGGAAAACA  
 TAATGATGTAATGCATCCTGATGGGAAGGCATGAGATGGGATTGTTAGAAGACAGAAGGAAAGACAGCCAT  
 AAATTCTGGCTTGGGAAAACCTCATATCCCCATGAAAAGGAAGAACATCACAAATAAAAGTGGAGACTATGAA  
 TGGAGCTTTCACTAGGGTATAAGTAGCTGCCAATTGTAATTCTGTTAAAAAAATCTAGATTTATAACCA  
 AACTGCTAGAAAATCTGAGGAACATAAATTCTCTGAGAACATAGGAAGAGTAGACATTGTTATTCTTACTGC  
 ATTGATTTCTCTGTATATTGGATTGTTGAGTATATTGAGTGAATAGGAGAAAACAATATAACACACAGA  
 GAATTAAGAAAATGACATTCTGGGAGTGGGATATATTTGTTGAATAACAGAACGAGTGTAAAATTAAAC  
 AACGGAAAGGGTAAATTAACTCTTGACATCTCACTCAACCTTCTCATTGCTGAGTTAATCTGTTGTAATT  
 GTAGTATTGTTTGTAAATTAAACAATAAAAGCCTGCTACATGT

**FIGURE 176**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLKLTYKDLLLSNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHFILLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSILGPTHDHHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDFKTLILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVYGVFTTSSIFKGSACVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVLE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHEADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRRHHRLDELPRAVAT

```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

## FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTATCCTGGAGCATGCCAACCGCGGGGAGCAGA  
 CAACCTCCCAGGTAAGCTGGAGCAAGACCTGAAGCTTCTCAGGAGCCTGGTGTATTTCCCCCACCCAC  
 CTCAGCAGTTCAGCCAGCAGGGACTGATCAGGTGTGCTCTGGAGTGGGAGCAGAAGGCCTGGCTGGCAAGA  
 GTGCCCTGGAGAAAGAGGTTCAGCGCTTGACCAGCGACTGCCGTGACTACAAGATCCAGAACCATGGGCATC  
 GGGTAGGGTGGGGGGCACAGGTGTATGTCACCTTCTGTCAGCAAGAAGAGCTGAGAGAGGGGATCTGG  
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGCACAATAGTTAA  
 GAGCACAGTTTGGAGCTAGACCGACATAGGGTCAAATTCTCTGTTCTAGTCTGTAGCCCCAGGT  
 AAGGGAGTGACTTAACCTCTGGACTTCATTCCTCATCACTAAAGTAGGGCAATAATAGCACCCACCTCAT  
 AGGAAGATTAAATGACATAATGTATGTG**ATG**CAACTAGCAAAGTACCAAGTCCATAGTAAGTCATGCCACAG  
 TATTTCACCCACCCCTGTTCTGCCTTCCAAACCAGGTACTGCAACGACTGGAGCAGAGGGGGCAGCAGGCTT  
 CAGAGCGGGAGGCTCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGAGCATCCGCCGGCACAGGTGAGCC  
 AGGTGAAGGGGCTGCCGGCTGGCCCTGCTGCAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGGGCGGCTCAGTGAGGCTCGGCTGTCAGGAGCTTCCAGAGGGACCTCTC  
 CAACCGCTGAGGATGCTGAGCTTCTGACTTGAGGAATGTGAGGAGACGGGAGAGCTTTGAGGAGCCTGCC  
 CCCAAGCCCTGGCACAGAGGCCCTCCCTGCCCTGCACACGTGGTATTCGCTATCAGGAGGGCGTAGGATG  
 AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTATAGAGGAGGAGATGCTGACGAATGGTCAAGGCTCGGA  
 ACCAGCACGGCGAGGTAGGCTTGTCCCTGAGCGATATCTCAACTTCCCGACCTCTCCCTCCAGAGAGCAGCC  
 AAGACAGTGACAATCCCTGCGGGCAGAGCCACAGCATCTGGCACAGGCCCTGTACAGCTACACCGGACAGA  
 GTGCAGAGGGACTGAGCTTCCCTGAGGGGCACTCATCCGTCTGTCGCCCCGGCCAAGATGGAGTAGATGACG  
 GCTTCTGGAGGGGAGAATTGGGGGCGCTGTTGGGTCTCCCTCCTGCTGGTGGAGAGCTGCTGGCCCC  
 CAGGGCCACCTGAACACTCTGACCTGAACAGATGCTGCCGTCCCCCTCTCTCCAGCTCTCCCCACCTGCAC  
 CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGCTGCCCTGGGACAAGCCCTGGACTTCCCTGGGTTCTGG  
 ACATGATGGCACCTGACTCAGGCCATGCGTCCACCACCTCCCCCGGGCTAAAGGCCGGATCTGGGCCACC  
 CAGATCCCCCACCT**TGA**AGGCCAGGGAAAGCCTGACCCCCAGTGTGCTGTCCTATCTCAAGCTGTCAGA  
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGAATGCCCTTATTCCACCTCACCTCCAAGGGT  
 GGAAACTTGCCCCTCCCATTCTAGAGCTGGAACCCACTCTTTTCTCCATTGTTCTATCATCTTAGGACC  
 GGAACACTACCTCTCTGTATGACCTATCTAGGGTGGTGAATGCCCTGAATCTCTGGGCTGGAAAC  
 ATCCATCAAGGTCTAGTAGTTCTGGCCACCTCTTCCCCACCCCTGGCTCCATGACCCACCCACTCTGGATG  
 CCAGGGTCACTGGGTTGGCTGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
 CTGTAATGGCTGAGCGGATTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCTTGTG  
 CTAAGAGGGCAGGGGCCCTACGGTGTATTGCTTAGGGGCCACCACGGGCAGGGCCTGCTCCAGTGCAC  
 GCTCTATCATATGGAGCGAGGTGTTGGGAAGCGGGGGCAGGCAGCCTGTTGCGAGCAGGGAAAGGAGAAGAGAC  
 TGAGGGCTGTGACCTCTCTGAGGCCACCTGAGACTGTCACCTCAGGTGGAAGTAGAGCTGGTCCCTC  
 AGCTGGGGGCAGTGTGCTCCAGTGGCTGGGAGGGCTTACGCCACCCACCCCTGGCCAGCTGGTAG  
 TCCATCAGCACCATGAAGGAGACTTGGAGAAGAGAATAACACTGTTGCTCTGTTCAAGCTGTGTCAGC  
 TTTCCCCCTGGGCTCCAGGACCTCCACCAACCAAGGGATTATAGCAAAGGCTAAGCCTG  
 AGTTACTCTGGGGTCAAGGAGCGAAAGGCTAAATAGTTAAGTAGGTGATGGGAAGATGAGATTACCTCA  
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG  
 TCAACAATGAGAGACCAAGAGGAGACTGAGCTGAGGAGCAGGAGCTGAGGAGCAATAAGAGCCAGGCCAGTGC  
 AGTCCCGGCTGTGTTCTACCTGGTGTACAGAAGTGTGCTGGTTCTGGCTGCCATTGCTCTGAGTGG  
 GCAGCCCTGGGTTAGGCTGCTCCCTGAGTCCTCATTCTGTACTGGGGCTGGCTAGGACCTGGGCTGTGGCC  
 TCTCAGGGGGCAGCCTCCATGGCAGGCATCCCTGCCCTGGCTGCCCTCCCCAGAGGCCATTGGCTGCTGAGTCC  
 GGTCTGTCCCCCACCAGAGCCCAAGCTCCTGTGTGGGGAGCCATCACGGTGTGCGAGTCCATAGCGCT  
 TCTCAATGTGTGTCACCCGAACCTGGAGGGAGGGAACACTGGGTTAGGACCAACACTCAGAGGCTGCTTG  
 GCCCTCCCCCTGACCAGGGACATCCTGAGTTGGCTACTTCCCTCTGGCTAAGGTAGGGAGGCCCTCTC  
 AGATTGTGGGCACATTGTTAGGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT  
 TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCACTGCC  
 CAGAGAACACAGTGGTCTCCCTGTCGGGGGGCGCTTTCCCTGGAGCGTCCCTGACGGACAAGTGGAG  
 GCCTTGTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGGCCAGGTGCACTGTTGATGATGGGAGGGGCTC  
 CGTCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGAGTGAGGGTAACATTCCATTCC  
 TCATGTTTGTCTTACCTCAGCATGCTCTTAAACCCAGAAGCCCCAATTCCCCAAGCCCCATT  
 TTTCTGTCTTATCTAATAACTCAATATTAAG

**FIGURE 178**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pi: 4.53, NX(S/T): 0
MQIAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRSIRRA
QVSQVKGAARLALLQAGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDAEW
VKARNQHGEVGFVPERYLNFPDLSLPESSQDSNPCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRGVFPSLLVEELLGPPGPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAKAPDPGHPDPLT
```

## FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGAAAGAGACAGAGACAAAGGCACAGCGGAA  
 GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGACTCCTACAGAGGGAGAGGCAGAGAAAGCTGCAGA  
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAGGAGGGCTCAGGAGGAGAGTTGGAGAAGCCAGACCCCTGG  
 GCACCTCTCCAAGGCCAAGGACTAAGTTCTCCATTCTTAAAGGTCCTCAGCCCTCTGAAAACCTTGC  
 TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTCCAAAGCTAGGGTGTGGAGGACTTGGT  
 GCCCTAGACGCCCTAGTCCCTCCCAGCTGCAGTACCAAGTGCATGCTCCAGACAGGCTCGCATCCGGGAGGG  
 CTTGGCAGGGCCTGGCTGGGGAGGCCAACCTGCCTCTGCTCCCCATTGTGCCGCTCTCTGGCTGGTGTG  
 GCTGCTTCTGTAUTGCTGGCCTCTCTGCCTCAGCCGGCTGCCAGCCCCCTCCCCGGAGGAGGAGAT  
 CGTCTTCCAGAGAAGCTAACGGCAGCGTCTGCCCTGGCTCGGGGCCCTGCCAGGCTGTGTGCCGTTGCA  
 GCCCTTGGGAGACGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGAGGGCTGACAGTGCAGTA  
 CCTGGGCCAGGCCTGAGCTGCTGGGTGGAGCAGACCTACCTGACTGGCACCATCAATGGAGATCC  
 GGAGTCGGTGGCATCTGCACTGGATGGGGAGCCCTGTTAGGGTGTACAATATCGGGGGCTGAACCTCA  
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGACCTGGGCTCACATCTACGCCGGAAAGAGTCC  
 TGCGAGCGGTCAGGTCCATGTCAACGTCAAGGCTCCTCTGGAAAGCCCCAGCCCCAGACCCGAAGAGCCAA  
 GCGCTTGGCTTCACTGAGTAGATTGTGGAGACACTGGTGTGGCAGATGACAAGATGCCGATTCCACGGTGC  
 GGGCTAAAGCGTACCTGTAACAGTGTGGCAGCAGCAGCAAGCCTCAAGCACCCAAGCATCCGCAATCC  
 TGTCACTGGTGGTGTGACTCGGCTAGTGTATCTGGGTCAAGGCAGGAGGGGCCCAAGTGGGCCAGTGTGC  
 CCAGACCCCTGCGCAGCTCTGTGCCCTGGCAGCGGGGCCCTAACACCCCTGAGGACTCGGGCCCTGACCACTTGA  
 CACGCCATTCTGTTACCGCTCAGGACCTGTGTGGAGTCTCACTTGTGACACGCTGGTATGGCTGATGTGGG  
 CACCGTCTGACCCGGCTGGAGCTGCCCCATTGTGGAGGATGATGGCTCCAGTCAGCCTCACTGCTGCTCA  
 TGAACCTGGGTATGCTTCAACATGCTCCATGACAACCTCAAGGCCATGCACTGATCAGTTGAATGGCCTTGTGAC  
 CTCTGCCATGTCATGGCCCTGTGTGATGGCTCATGGATCTGGGCTGGGCTGGCCCTGCACTGCCGCTT  
 CATCACTGACTCCTGGACAATGGCTATGGCCTGTCTTAGACAAACAGAGGCTCCATTGCATCTGCCCTGT  
 GACTTCCCTGGCAAGGACTATGATGCTGACGCCAGTGCACCTGCACTTGGGCCCCGACTCACGCCATTGTCC  
 ACAGCTGCCGCCCTGTGCTGCCCTCTGGTCTCTGGCACCTCAATGGCATGCCATGTGCCAGACCAAACA  
 CTCGCCCTGGGCCGATGCCACACCCCTGCGGGCCGACAGGCCATGGGTGGTCGTGCCCTCACATGGACCA  
 GCTCCAGGACTTCAATATCCACAGGCTGGTGGCTGGGCTCTGGGACCATGGGTGACTGCTCTGGACCTG  
 TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCACGAGGCCCTGTCAGGCTGTGGTGTCCAGGGCGATGCATCCATGCTGG  
 CCGCCGTACCGCTTCCGCTCTGCAACACTGAGGACTGCCAAGTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
 GTGTGCTGCCATCACACCACCGCACCGACCTCTCAAGAGCTCCCAGGGCCATGGACTGGGTTCTCGCTACAC  
 AGGGTGGCCCCCAGGACCAAGTGCACACTCACCTGCCAGGCCGGACTGGCTACTACTATGTGTGGAGCC  
 ACGGGTGGTAGATGGACCCCTGTCCCCGGACAGCTCTGGTGTGTGGTGTCCAGGGCGATGCATCCATGCTGG  
 CTGTGATCGCATCATTGGCTTCAAGAAGATTGACAAGTGCATGGTGTGGAGGGGACGGTTCTGGTTGCA  
 CAAGCAGTCAGGCTCTTCAAGGAAATTCAAGGTACGGATACAACAATGTGGTCACTATCCCCGGGGGCCACCCA  
 CATTCTGTCCGGCAGCAGGGAAACCTGGCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCTA  
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGAGTCAGCTGCGCTA  
 CAGGGGGCCACTGCAAGGCCACTGTCAGAGACACTGTCAGGCCATGGCACTGGCCAGCCTTGTACACTGCAAGTC  
 AGTGGCTGGCAACCCCGAGCACACGCCCTCCGATACAGCTCTCGTCCCCGGCGACCCCTCAACGCCACG  
 CCCACTCCCCAGGACTGGCTGCCACGGAGACAGATTCTGGAGATCTTCCGGCGGCCCTGGCGGGCAG  
 GAATAAACTCACTATCCGGCTGCCCTTCTGGCACCGGGCTGGACTTAGCTGGAGAAAGAGAGAGCTT  
 CTGTTGCTGCCCTATGCTAAGACTCAGTGGGAGGGCTGTTGGAGGAGCCTGGCCCTCTCTGCCCTAAT  
 GCGCAGGCTGGCCCTGCCCTGGTTCTGCCCTGGAGGAGCAGTGTGGTTAGTGGATGGAAGGGGCTGACAGAC  
 AGCCCTCCATCTAAACTGCCCTCTGCCCTGCCCTGGGAGGAGCAGATCTGGAGATCTTCCGGCGGCCCTGGGCC  
 CAGTGTATTATTAGTATTACTTCTTTATTAGCACCAAGGGAAAGGGACAAGGACTAGGGTCTGGGAA  
 CCTGACCCCTGACCCCTCATGCCCTCACCTGGGCTAGGAAATCCAGGGTGGTGTAGGTATAAGTGGT  
 TGTGTATGCGTGTGTGTGTGAAAATGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTC  
 TTGCTGAAATTATTAGTATTACTTCTTTCTTTCTTTGAGACAGAACTCGCTCTGTCGCCAGGCTGGAGTGC  
 GCACAACTCGGCTCACTGCATCTGCCCTCCGGTCAACTGATCTCATGCCCTAGCCTCTGAGTAGCTG  
 GGATTACAGGCTCTGCCACCACGCCAGCTAATTGTTGTTGTTGGAGACAGAGTCTCGCTATTGTC  
 ACCAGGGCTGGAATGATTCACTGCACACCTGCCACCTGGGCTCAGCAATTCTCTGCCCTAGCCTCC  
 CGAGTAGCTGAGATTATAGGCACCTACCACGCCGGCTAATTGTTGTATTAGTAGAGACAGGGTTTC  
 CATGTTGGCCAGGCTGGTCTGAACTCTGACCTTAGGTGATCCACTGCCCTCATCTCCAAAGTGTGGATT  
 ACAGGGCTGAGCCACCGTGCCTGGCACGCCAACTAATTGTTGTATTAGTAGAGACAGGGTTTCA  
 TGGCAGGCTGCTTGAACCTCTGACCTCAGGTAACTGACACTGCCCTGGCTCCAAAGTGTGGATTACAGG  
 TGTGAGCCACCAAGGCCGGTACATATTAAATTGAATTCTACTATTATGTGATCCTTGGAGTCAGACAG

**FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTCTCATTGCCAATAATAATACCTCCCTAGAAG  
TTTGTGAGGATTAATAATGTAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGAAAA  
AAAAAAAAAAAAAAAAGAAAAAAAAGAAAAAAAAGAAAAAGAAA

## **FIGURE 180**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSGAPARLLCRLQAFGETLLEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINGDPESVASLHWDGGALLGVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFASLSRFETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRILVILGSGEEGPQVGPSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDFPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRRHMAPVMAHVDPPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PTVFPGKDYDADRCQLTFGPDSRHCQLPPPACAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCILHMDQLQDFNI PQAGGWGPWGPWGDCSRTCAGGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMWDWVPRYTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK

```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 358-367

## FIGURE 181

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**  
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCC  
 AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT  
 AATTGTCCTGTTGGGGAGCAAGCAGTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG  
 ACCAGAACTGAAATATTCAAGAGCGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
 TAAAAACGGATACACTGGCATCTACTCGTGGGTCTTCAAAATGTTTATCAAAACTCAGA  
 TTAAAGTGATTCTGAATTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
 ACAACTTTCTTGAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
 TTTCTTAAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC  
 CCACTCTAATATCAGTTCTGAGTTACAAGACTTGAGGAGGGAGAAGATCTTCACTTT  
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAGT  
 AGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGAAGAACTCCAATAATGACTATACTG  
 AAAATGGAATAGAATTGATCCATGCTGGATGAGAGAGGTTATTGTTGTATTACTGCCGT  
 CGAGGCAACCGCTATTGCCGCCCGTCTGTGAACCTTACTAGGCTACTACCCATATCCATA  
 CTGCTACCAAGGAGGACGAGTCATCTGCGTGTACATGCCCTGTAAGTGGTGGTGGCCC  
 GCATGCTGGGAGGGC**TAA**AGGAGGTTGAGCTAAATGCTAAACTGCTGGCAACATAT  
 AATAAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT  
 CTCCAGAATTACTGTAGGTAATTCTCTCTCATGTTCTAATAAAACTTCTACATTATCACC  
 AAAAAAAAAAAAAAAA

**FIGURE 182**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLLIVLFWGSKHFPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTFEEQSVIWWPAEKPIENRDFLKN SKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHF PANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMELDERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV

```

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 183**

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGCGTGACCCGAGGGCCAGGGAGCTGCC  
 CGGCTGGCCTAGGCAGGCAGCCGCACCAATGGCCAGCACGGCGTGCAGCTCTGGGCTTCCT  
 GCTCAGCTTCTGGCATGGTGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGCACCAACATCCTCACGGCGTGTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
 GCGCCTGCCCGTCATCGGATGAAGTGCACCGCTGCCAAGGGCACACCCGCCAAGACC  
 ACCTTGCCATCCTCGCGGCACCCCTTCATCCTGGCCGGCCTCTGTGCATGGTGGCGT  
 CTCCTGGACCAACGACGTGGTGCAGAACTTCTACAAACCGCTGCTGCCAGCGGCATGA  
 AGTTGAGATTGCCAGGCCCTGTACCTGGCTTCATCTCCTCGCCCTCTCGCTCATTGGT  
 GGCACCCCTGCTTGCCCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCGCC  
 CAGGGCCACACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
**TGA**GTCCCCACAGCCTGCTTCTCCCTGGCTGCTGTGGCTGGGCTGGGCCCCGGCGGACTGTC  
 AATGGAGGCAGGGTTCCAGCACAAAGTTACTTCTGGCAATTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAAGACTGAAAAAAATCCTGTCTGTTTGTATTTATTATATATAT  
 TTATGTGGGTGATTGATAACAAGTTAATATAAGTGACTTGGGAGTTGGTCAGTGGGT  
 TGGTTGTGATCCAGGAATAAACCTTGCAGATGTGGCTGTTATGAAAAAA

## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGLTITLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ  
DEAPYR PYQAPPRATTTANTAPAYQPPAAYKDNRAPS VTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

## FIGURE 185

GAGCTCCCTCAGGAGCGCTAGCTCACACCTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
 CAGGCGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACATGCCAAGTGGTGGCGTTCCCT  
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGCCACCAGGATGGACATGTGGAGCACCC  
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
 GTGAGGCAGAGTTCAGGCTCACCGAATGCAGGCCCTATTCACCATCCTGGGACTTCCAGC  
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC  
 TGGTATCCATCTTGCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGGATCATGTTCATTGTCTCAGGTCTTGTCAATTGCTGGAGT  
 GTCTGTGTTGCCAACATGCTGGTACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGCAGGCTCTGGTGTG  
 GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGG  
 CCTGGCACCAAGAACCAACTACAAAGCCGTTCTTATCATGCCCTCAGGCCACAGTGTG  
 CCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTTGGGTCCAACACCAAAAACAAGAAG  
 ATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTTATCCTCCAAGCACGACTA  
 TGTG**TAAT**GCTCTAACACCTCTCAGCACGGGCGGAAGAAACTCCGGAGAGCTCACCCAAAA  
 AACAAAGGAGATCCCCTAGATTCTTCTTGCTTTGACTCACAGCTGGAGTTAGAAAAGC  
 CTCGATTCATCTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTGTCTCTAAATATTCC  
 ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCATCCTCTAT  
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTAATCTCTCTCAC  
 ATTTGATGATTTAGACAGACTCCCCCTTCCTCCTAGTCAATAAACCCATTGATGATCTA  
 TTTCCCAGCTATCCCCAAGAAAACCTTGAAAGGAAAGAGTAGACCCAAAGATGTTATT  
 CTGCTGTTGAATTGTCTCCCCACCCCAACTGGCTAGTAATAAACACTTACTGAAGAA  
 GAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGCCCATGATCTGGTTCTTACACTG  
 TGATCTAAAAGTTACCAAACCAAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTG  
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG  
 TCCTCTTCTGTCGGGGTCAGAAATTGCCCTAGATGAATGAGAAAATTATTTTTAAT  
 TTAAGTCCTAAATATAGTTAAAATAATGTTAGTAAAATGATACACTATCTCTGTGA  
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT  
 ATATGGTACTTTGTAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC  
 CTAGCACTTGGGAGGCTGAGGAGGAAGGATCACTGAGGCCAGAAGTTCGAGACTAGCCTG  
 GGCAACATGGAGAAGCCCTGTCATACAAATACAGAGAGAAAAATCAGCCAGTCATGGTG  
 GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGAGGATCACTGAGGCCAGGG  
 AGGTTGGGCTGCAGTGAGCCATGATCACACCACTGCACCTCAGCCAGGTGACATAGCGAGA  
 TCCTGTCTAAAAAATAAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA  
 ACTAATTCTTAA

## **FIGURE 186**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTS
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## FIGURE 187

GGAAAAACTGTTCTCTCTGTCGGCACAGAGAACCCCTGCTCAAAGCAGAAGTAGCAGTTCCG  
 GAGTCAGCTGGCTAAAACATCCCAGAGGATA**ATG**CAACCCATGCCTTAGAAATCGCTG  
 GGCTGTTCTGGTGGTGGAAATGGTGGGCACAGTGGCTGTCACTGTCAATGCCCTCAGTGG  
 AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG  
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
 CTCTTCTCCGGACCTACAGGCAGCAGAGGACTGATGTGCTGCTCCGTGATGTCCTTC  
 TTGGCTTCATGATGGCCATCCTGGCATGAAATGCACCGAGGTGCACGGGGACAATGAGAA  
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCACGGCATGGTGGTGC  
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT  
 GTTGCCCAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCACTGGTGCT  
 GATTGTTGGAGGAGCTGTTCTGCTGCGTTTTGTTGCAACGAAAAGAGCAGTAGCTACA  
 GATACTCGATACTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG  
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTATGTTTTAACTTTACTATAAAGC  
 CATGCAAATGACAAAAATCTATATTACTTCTCAAATGGACCCAAAGAAACTTTGATTAA  
 CTGTTCTTAACTGCCTAATCTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA  
 GCTATTCAGCAGAATGAGATATTAAACCAATGCTTGATTGTTCTAGAAAGTATAGTAAT  
 TTGTTCTAAGGTGGTTCAAGCATCTACTCTTTATCATTACTTCAAATGACATTGCT  
 AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG  
 TGTAACATTATCTCACATAGAGACATGCTTATGGTTTATTAAAATGAAATGCCAG  
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGGTTG  
 AAGAAGGTTACTATTAAATTGTTAAAACAGCTAGGGATTAATGTCCTCCATTATAATGA  
 AGATTAAAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG  
 TTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATCCTCTCCAGAGGCTTTTT  
 TTCTTGTGTTAAATTAAACATTAAAACGCAGATATTGTCAGGGCTTGCATTCA  
 AACTGCTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTG  
 GTTTAGGAAAGTGAATAATTGTTTGTGTTGTTGTTGAGTACAGACTTGAGGTTCATC  
 GAAATCATATGTGATGGATATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATC  
 AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTCATTGCTTACCAAAAAACAAACA  
 ACAAAAAAAAGTTGTCCTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTC  
 AAAATTGTCATTGTTCTGTGAAAAATAATTCCCTTGTACCATTTCTGTTAGTTACTAAA  
 ATCTGTAAATACTGTATTCTGTTATTCCAAATTGATGAAACTGACAATCCAATTG  
 AAGTTGTGTCGACGTCTGTCTAGCTAAATGAATGTGTTCTATTGCTTATACATTATA  
 TTAATAAATTGTACATTCTAATT

## **FIGURE 188**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## FIGURE 189

TCGCC**ATG**CCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGCTGGGTG  
 AATGGCCTGGTCTCCTGTGCCCTGCCATGTGGAAGGTGACCGCTTCATCGGCAACAGCAT  
 CGTGGTGGCCCAGGTGGTGTGGAGGGCCTGTGGATGTCTGCCTGCGTGGTGCAGAGCACCGGCC  
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
 GCCCTCTGTGTCATGCCCTCCTGTGGCCCTGTCGGCTTGTGGTCTACCTGCTGGGC  
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCGCCGGTGCACCTCTGGGA  
 TTGTCTTGTCATCTCAGGGGTCTGACGCTAACCGCTGTGCTGGACGGCGATGCCATC  
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCAAAAGCAGGGAGCTGGGGCCTCCCT  
 CTACTTGGGCTGGCGGCCCTCAGGCCTTTGTTGCTGGTGGGGGGTTGCTGTGCACCT  
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT  
 GCCATCTCTCGGGGGCCCTTGAGTACCCCTACCAAGAATTACGTC**TGA**CGTGGAGGGGAATG  
 GGGGCTCCGCTGGCGCTAGGCCATCCAGAAGTGGCAGTGCCAACAGCTTGGATGGGTT  
 CGTACCTTTGTTCTGCCTCCTGCTATTTCTTTGACTGAGGATATTAAAATTCAATT  
 GAAAATGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTCTCACCTTGG  
 ATGATGGAGCCAAGAGGGATGCTTGAGATTCTGGATCTTGACATGCCATCTAGAAC  
 CAGTCAGCTATGAACTAATGCGGAGGCTGTTGCTGTGCTGGCTTGCAACAAAGACAGAC  
 TGCCCCAAGAGTTCTGCTGCTGGGGCTGGCTCCCTAGATGTCAGTGACAGCTG  
 CCCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTCACCCCTGGAAAAACAAATCATCTG  
 TTAACAAAGGACTGCCACCTCGGAACCTGACCTCTGTTCTCCGTGATAAGACG  
 TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
 CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG  
 TTTGTTAGTGCA

## **FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLGVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTS
FVISGVTLIIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLCCTCP
SGGSQGPGSHMARYSTSAPAIISRGPSEYPTKNYV
```

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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## FIGURE 191

GCCAAGGAGAACATCATCAAAGACTCTAGACTCAAAAGGCTCCACGTTCTACATCTG  
 AGCATCTTCTACCACTCCGAATTGAACCAAGTCTCAAAGTAAAGGCAATGGCATTATCCC  
 TTGCAAATTGCTGGCTGGTCTTGGGCTTGGCATGGTGGGGACTCTGCCACAACCCT  
 TCTGCCTCAGTGGTGGAGTATCAGCTTGTTGGCAGAACATTATTGTCTTGAGAGGCTC  
 TGGGAAGGGCTCTGG**ATG**AATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
 TAGCTCCTTGTTGGCTCTCCGCCTGCCCTGGAAACAGCCCAGGCCCTATGTGTGGCTG  
 TTGCTCTCTCCTTGATGCCCTGCTTATTGGCATCTGGCATGAAGCAGGTCCAGTGCACA  
 GGCTCTAACGAGAGGGCAAAGCATACTTCTGGAACTTCAGGAGTCCTTCATCCTGAC  
 GGGTATCTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA  
 ACCCAGCCATCCACATAGGTAGAACGAGAGCTGGAGCAGCACCTTCCTGGCTGGCA  
 AGCGCTGCTGTCCTCTCATTGGAGGGGTCTGCTTGTGGATTTGCTGCTGCAACAGAAA  
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTC**TAA**TGCCTCCTTGCTCCAAGT  
 ATGGACTATGGCAATGTTTATAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
 GAACTTGCTTATGTCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG  
 AATGAAAATGACTTACTGGACATTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
 GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
 TGTACAATGATGGACTACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
 GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

## **FIGURE 192**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

## **FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATG**AAGATCACTGGGGT  
CTCCTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCTGCCCATCA  
CATACCTACCAGTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTCAGTTCTCACGATGGAAGTTGC**TAA**ATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTCATCCCAGGCTCTGACTG  
AGTTCTTCAGTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGTAATCTTG  
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

## FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

**Signal peptide:**

amino acids 1-19

**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTGCCCTGCTCGCGCCC  
CGCCGCCATGGCTGCCTCCCCCGCGCCCTGCTGCTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGCCAGGTGGCATAAGTGGAAATAACTCAAGCTGATGCTCAA  
AAACGAGAACGACCTGTTCCAACTAAGACTAAAGTGGCGTTGATGAGAATAAGCCAAAGA  
ATTCCCTGGCAGCCTGAAGCGCCAGAACGGCAGCTGTGGGACCGGACTCGGCCGAGGTGC  
AGCAGTGGTACCAGCAGTTCTACATGGCTTGATGAAGCGAAATTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACTAACCATGACTGCCACACGCTGTACAAGAACAAATAGCGATT  
TCTTCATGTATCTCTTAATGCCTTACACTACTTGGTTCTGATTGCTCTATTCAGCAGAT  
CTTTTCTACCTACTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGAAATGCCTT  
TGATATTCATGGGAATGCCTCTCATTAAAAATAGAAATAAGCATTGTTAAAAAGA

## **FIGURE 196**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLCWGP GGISGNKLKMLQKREAPVPTKTKAVDENAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEY YGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY
```

**Signal peptide:**

amino acids 1-30

**FIGURE 197**

CGGCTCGAGCCGCCCGGAAGTGCCGAGGGGCCGATGGAGCTGGGGAGCCGGCGCTC  
 GGTAGCGCGGCGGGCAAGGCAGGCATGACCTGATTGAAGGGTGGGTATGAGGTGAC  
 CGTCCTTCTCGGTGCTTGCCTGCCTCTGGTGCAGGCCCTGCCTGGTCTAACGCACA  
 CCGCTGAGGGCGGGACCCACTGCCAGCCGTAGGGACCCAACGCCATCCCAGCCAGC  
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT  
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGTTCACAGAACACCGCCAG  
 CCCCGACTCCCCCAGGAGCCCTCGTGCAGGCTGAAATTCCCTCAATGATTAGCAGAGCAG  
 GTGGCCAGGGCTGGCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTCCGGCG  
 GGAAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCAGCACCCAGACCCCTGG  
 GCAGCCTCACCTCCCTCCAACTGCCTCTCCACTGCCACGTGCTCCACGAGAGTCGGTCCC  
 CCAAATCCCCCTGCCGCCGGGTCCGAGCCCGCCCTCCGGCTGGAAATGGCAGCCT  
 GCTGCTGCCCTGCTCCTGCTGTTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
 CCTTCTTCCCTGACCGCCACTCTGGCCTGGCCGGCTCACCTGCTCCTCAGTCCTG  
 GCCTTGCCATGTACCGCCGTAGGCCTCCGGCGCTTGGCAGCGTCGCCGGCCCTCC  
 GGACCTTGCTCCCCGCCGCCGGAGCTGCTGCCTGCCAGGCCGCCTCTCCGGCTG  
 CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCCAGAGGACTCCGGGACTGGCGGAGG  
 CCCGCCCTGCGACGCCGGGCTCGGGCACCTCCGGGCTGCTGAACCTCAGCCCGCA  
 CTGGGAGTGGGCTCCTCGGGTGGGCATCTGCTGTCGCTGCCTGGCCCGGGCAGAGCCG  
 GGCGCCCCGGGGCCGTCTAGTGTCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC  
 AGCTCCTTGGGCTGAGTTGGGACGCCAGGTGGCTGGAGGCTGGTAAGGGAGCGGGGAG  
 GGGCAGAGGAGTTCCCCGGAACCGTGCAGATTAAAGTAAGTGAAGTTAAAAAAAAAA  
 AAAAAAAA

## **FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS  
EPGPGSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLLSSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCCTAAGAACCATCAGCCC  
TCAGCTGCACCTCCTCCCTCCAAGGATGACAAAGGCCTACTCATCTATTGGTCAGCAGC  
TTTCTTGCCTAAATCAGGCAGCCTCATCAGTCGCTGTGACTTGGCCCAAGGTGCTGCAGCT  
GGAGGACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG  
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTGACTATGCCCTC  
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTGCCA  
CGTAGACTGTCAAGATCTGCTGAATCCAACCTTCTTGCAAGGCATCCACTGCGAAAAAGGA  
TTGTGTCCGGAGCACGGGGATGAACAACTGGTAGAATGGAGGTTGCACTGTTCAGGCCGG  
CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGATGAAACAGGGTGCAGGTGCACCGTGG  
AGTCATTCCAAGACTCCTGCTCCTCAGGGATTCTCATTCTTCTTCCACTGCCTCCA  
CTTCATGTTATTTCTTCCCTCCATTACAACAAACTGACCAGAGCCCCAGGAATAAA  
TGGTTTCTGGCTTCCTCCTACTCCATCTGGACCCAGTCCCTGGTTCTGTCTGTTAT  
TTGTAAACTGAGGACCACAATAAGAAATCTTATATTATCG

## FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCHVDCQDLLNPNLLAGIHCAKRIVSGARGMNN
NWVEWRLHCSGRPLSYWLTGCRLR
```

### Signal peptide:

amino acids 1-18

## **FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGGAAAGAAACACCTGAG  
 CAGAATGGAATCATTATTTTCCCAAGGAGAAACCGGGTAAAGGGAGGGAAGCAATT  
 AATTGAAAGTCCCTGTGAATGGGCTTCAAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC  
 TTGGGGTGAACATTGGGTCTGTGGTTCTGATTGTAAGTGGAAAGCAGGTCTGCACACGC  
 TGTTGGCAAATGTCAGGACCAGGTTAAGTGAATGGCAGAAAAACTCCAGGTGGAACAAGCA  
 ACCCATGTTCTGCTGCAAGCTTAGCAACATGCTCTTAAGGAAGCGATAACAGGCACAGACATGAC  
 CTGTTGCATTGGCAAGTTCTAGCAACATGCTCTTAAGGAAGCGATAACAGGCACAGACATG  
 CAGACTCCAGTCCTCCTGCTGCTCCTGATGCTGGATGCGTCCTGATGATGGTGGCGATGT  
 TGCACCCTCCCCACCAACACCCCTGCACCACTGACAGACTGTCACAGCCCAAGCCAGCAAGCACAGCC  
 GAAGCCAGGTACCGCCTGGACTTTGGGAATCCCAGGATTGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTATCTCACTGCGGGAGGATCAGC  
 TGCTGGTGGCGTGGCCTACCCCAGGCCAGAAGGAACAGAGCAGGGCAGGAGAGGTGG  
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGAGATAAGGAAGGCCAAAGAGGGACTGGGG  
 GGCTGATGAGGACGGGGAGGTGTCAGAAGAAGAGGAGTTGACCCCGTTAGCCTGGACCCAC  
 GTGGCCTCCAGGAGGACTCAGTGCCGCATCCCCCTCCAGAGGGCTCTGCCAGGGTGC  
 CACCCACTGTGTCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
 CCAGGGCCTTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACACTCAAG  
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCGATGCTGGGGGCCACCAGAGCCACCGGGATGTGCTCGTCT  
 TCATGGATGCCACTGCGAGTGCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTATAGATGTGATTGACTGGAAGACTTCCAGTA  
 TTACCCCTCAAAGGACCTGCAAGCGTGGGTGTTGAAAGCTGGATTCCACTGGGAAC  
 CTTTGGCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG  
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCAAAACACTGGAGCGTATGACTC  
 TCTTATGTCGCTGCGAGGTGGTAAAACCTCGAACACTGTCCTTCAAGGCTGGCTCTGGT  
 GCTCTGTTGAAATCCTCCCTGCTCTGGTAGGACACATCTACAAAATCAGGATCCCCAT  
 TCCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTCGATTGCTGAGACCTGGCTGG  
 GTCATTCAAAGAAACCTCTACAAGCATAGCCCAGAGGCTTCTCCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTGCAAGCTGAAAGGAGACTGGTTGTCGGACATTCCACTGG  
 TTTCTGGCTAATGTCACCCCTGAGCTGACCCATCTGAACCCAGGCCAGTTCTGGAAA  
 GCTCCACAAACACTGGACTTGGCTCTGTGCAGACTGCCAGGAGAAGGGGACATCCTGGCT  
 GTCCCAGGTGTTGGCTCTGCACTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
 AGGAAGGAGATTCACTTGGCAGCCACAGCACCTGTGCTTGTGTCAGGCAGGAGCAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCCCTGGCCATCCACCAAGCAGCACTGGACTTCCAGG  
 AGAATGGGATGATTGTCACATTCTGGAAATGCATGGAAGCTGTGGTGAAGAAAAC  
 AATAAAGATTGTAACCTGCGTCCGTGATGGAAAAGGCCGCCAGCAGTGGCGATTGACCA  
 GATAAATGCTGTGGATGAACGAATGTCAGAAGAAAAGAGAATTGGCCATC  
 AAAATCCAGCTCCAAGTGAACGTAAGAGCTTATATATTGAAAGCTGATCCTTTGTGT  
 GTGTGCTCCTGTGTTAGGAGAGAAAAAGCTTATGAAAGAATAGGAAGTTCTCCTT  
 TCACACCTTATTCATTGACTGCTGGCTGCTTA

**FIGURE 202**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLMLGCVLMVAMILHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEYEYSPLEGGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDVTPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDLVFMADCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFOYYPSKDLQRGVLDWKLDFHWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIFYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEPDCMERLQLQRLGCRTFHWFLANVPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGLDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQQVILQNCTEEGLAIHQHQHWDFOENGIVHILSGKCMEAVVQENNKLILRPC
DGKARQQWRFDQINAVDER
```

**Signal peptide:**

amino acids 1-28

## FIGURE 203

CGCCAAGCATGCAGTAAAGGCTAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGA  
GTCCAGGATGTGCCCTGCGCTGCTGCTGCCACCTCCCTCTGGCCACTGCTGTGC  
TGCCCCCTCCCACCGCTGCTCAGGGCTCTCATCTCCCCCTCGAACCCCACCAGCCCCAGCC  
CGCCCCCCCCTGTGCCAGGGAGGGCCCTCGGCCACACGTATGTGTGCGTGTGGAGCGAGC  
ACCTCCACCAAGCCGATCTCTCGGGTCCCAAGATCACGTGGCAAGTCCCTGCCACTGG  
CACCCCCAGCCACCCCATCAGGCTTGAGGGAGGGCCGCCCTCATCCAAATACCCCTGGGCT  
ATCGTGTGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCC  
ATTTCTGGACTATGGTTGAGCCCCCTCATGGGCTCGAACCCCACACCCCAACTCAGACT  
CCATGCGAGGTGATGGAGATGGGCTTATCCTGGAGAGGCACCTGCCACCCCTGCCATT  
CTGTTGGGGGCCGTGGGAAGGTGTGGACCCCCAGCTATGTCACAATTACCATCTCC  
CATCATTGTTCTCGTGGCCACTGGCATCATCTCAAGTCTGCTGGGACCGCAGCCAGAAC  
GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA  
GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGCCTCGGGACTCACCTACCCCCACCC  
TGACCATGAGGAGCCCCGAGGGGACCCGGCTGGATGCCAACCCAAAGGGGCTCCAG  
CCTTCAGTTGAACCGGTGAGGGAGGGCAATGGATGGGAGGGCAAAGAGGAAGGCAAC  
TTAGGTCTTCAGAGCTGGGTGGGGTGCCCTCTGGATGGTAGTGAGGAGGCAGGCGTGGC  
CTCCCACAGCCCCCTGCCCTCCAAGGGGCTGGACCAGCTCTCTGGGAGGCACCCCTTC  
CTTCTCCAGTCTCAGGATCTGTGCTTATTCTGCTGCCATAACTCCAACCTGCC  
TCTTGGTTTTCTCATGCCACCTGTCTAAGACAACCTGCCCTCTAACCTGATTCCC  
CCTCTTGCTTGAACCTCCCTCTATTCTGGCTACCCCTGGTCTGACTGTGCCCT  
TCCCTCTCCTCTCAGGATTCCCCCTGGTAATCTGTGATGCCCAATGTTGGGTGCAGCC  
AAGCAGGAGGCCAAGGGCCGGCACAGCCCCCATCCACTGAGGGTGGGCAGCTGTGGGA  
GCTGGGGCACAGGGCTCTGGCTCTGCCCTTGACACCACCCGAACACTCCCCAGCC  
CCACGGCAATCCTATCTGCTGCCCTCTGCAGGTGGGGCCTCACATATCTGTGACTTC  
GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTGACACTCACCTCACCT  
AGGCCATTGACACGCTCTGCACCCCTCCCCGTCACCGCTCCGCTCAGCTGACTCT  
CATGTTCTCGTCTCACATTGCACTCTCCTCTCCACATTCTGTGCTCAGCTCACTCAG  
TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCGTTCCGGCTGATGTTGGTGG  
TGTGCGGCGTGCCTACTCTCTCCCTCATGAACACCCACCCACCTCGTTCCGCAGCC  
GTGCTGCTCCAGAGGTGGTGGAGGTGAGCTGGGGCTCTGGGCCCTCATGGTCA  
TCTCGTCCCATTCCACACCATTGTTCTCTGTCTCCCATCCTACTCCAAGGATGCC  
TCACCCCTGAGGGCTCCCCCTGGGAATGGGTAGTGAGGCCAGACTCACCCCCAGCC  
CTGCTAAAATCTGTTCTGACAGATGGGTTTGGGAGTCGCCTGCTGCACTACATGAGAA  
AGGGACTCCCATTGCCCTCCCTTCTCTCACAGTCCCTTGTCTTGTCTGCTG  
TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCC  
CCCTTGGGCCCTCCCTAACCTCCACCTAGGCTGCCAGGGACGGAGTCAGCTGG  
ATCGGGAGCTGCCTCCAAGTCTACCCCTCCCTCCGGACTCCCTCTGTCC  
CCTCCCTCTCCCTCCACTCTCCCTTGTCTTGTCTGCCCTTCCCCCTCAGG  
CTTCCCTCTCTCACTGGTTTCCACCTCCTCCCTTGTCTTGTCTG  
GTGATATATATTTGTATTATCTCTTCTTCTGTGGTGA  
GGATGTAAGTTCAAAATTCAAAAGCCTTGCAAGATAA

## **FIGURE 204**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRSSVEGLCEGIGAGLVDVAVWVGTCSDYPKGDASTGWNSVSRIIIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 205**

GTAAACCAGCGCAGTCCTCCGTGCGTCCGCCGCGCTGCCCTCACTCCCGGCCAGGATGG  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCGAGCTGCC  
GTCGGGAGAAGGCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCCCTGGACACCGGTCCCC  
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCAGGGCTGGACCAGGGC  
GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTATGCCGCCCTGCTGGCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTCTGCCTCCTGAAGCGAATAAA  
GGGGCCGCGCCGGCCGCGCGACTCGGCAAAAAAAAAAAAAAA

## **FIGURE 206**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREGPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristylation site.**

amino acids 91-96

## **FIGURE 207**

GGCGTGGTGGTGGCGCGGCTGAAGGGTGTGGCGAGCAGCGTCGGTGGCGCG  
 CGGGCCGGGACGGGCATGGCCCTGCTGCTGCCCTGGTGTGCCCTGACGGCGCGCTGGCCA  
 CGGCTGTCTGCACTGCCACAGCAACTCTCCAAGAAGTCTCCTCTACCGCCACCATGTGA  
 ACTTCAAGTCTGGTGGGTGGCGACATCCCCGTGTCAGGGCGCTGCTCACCGACTGGAGC  
 GACGACACGATGAAGGAGCTGCACCTGGCATCCCCGCCAAGATCACCCGGAGAAGCTGGA  
 CCAAGTGGCGACAGCAGTGTACAGATGATGGATCAGCTGTACCAAGGGAAAGATGTACTTCC  
 CCGGGTATTCCCCAACGAGCTGCGAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGAGGAGGGCAGCTCTCCAGGGAGGG  
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCCTAAGTAGCCC  
 CCAGAGGCCTGGGAGTGTGCCACGCCCTCCCTGAAGTTGCTCCATCTCACGCTGGGG  
 GTCAACCTGGGGACCCCTCCCTCCGGGCATGGACACACATACATGAAAACCAGGCCGCAT  
 CGACTGTCAAGCACCGCTGTGGCATCTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG  
 ACTCGCACGTGCCCTGTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCGT  
 GCCAGGGCCCTACTGTCCCTGGGCTCCAGGCTCTCCTGGAGGGGCTCCCGCCTTCCAC  
 CTGGCTGTCACTGGGTAGGGCGGGGCGTGGGTTCAAGGGCGCACCACCTCCAAGCCTGTGT  
 CCCACAGGTCTCGCCGCAGTGGAAAGTCAGCTGTCCAGGGCCTCTGAACATACATAAAAC  
 TGGCACAAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGT  
 GGTGAGTATGTGTGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCTAGAGGGCTCCGA  
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGCTGCAGTCCTTCTCCCTCAAAG  
 GTCTCCGACCCCTCAGCTGGAGGCGGCATCTTCTAAAGGGTCCCCATAGGGTCTGGTCC  
 ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTCCCTACGATGGTTAGGGGTGCC  
 ATGGAGGGCTGACTGCCACATTGCCCTTCAGACAGGACACGAGCATGAGGTAAAGGCC  
 CCTGACCTGGACTTCAGGGGGAGGGGTAAAGGGAGAGAGGAGGGGGCTAGGGGTCC  
 AGATCAGTGGGGCACTGCAGGTGGGCTCCCTACCTGGACACCTGCTGGATGTCAC  
 CTCTGCAACCACACCCATGTGGTGGTTCATGAACAGACCCACGCTCCTGCTGCC  
 CCTGGACACACAGAGCCACCCCGGCCCTGTGAGTGAACAGAGGAGGAGGGCTCGGAGA  
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCAGGGCTGCACACCCCTCGGACATCCCAGG  
 ACGAGGGTGTGATGTGCCACACATAGGACACACAGTCCAGCTGGAGGAGAGGC  
 GGGGCCAGGGAGGGAGGCAGGGGGTGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
 CCGCAGCCTGGTATGCCAGCCTAACGGTGTCTGGAGCCCCACACTGGCAACCTGACCT  
 TGGAAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGCCTGCCAGGG  
 GTGGGGCGGAGACTCAGCTGGACAGCCCTGCCACTCTGGAGCTGGCTGCTGCTGC  
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCAGGAGGGCGGAGG  
 GAGGGAAATGGGGTGGCTGTGCGCAGCATCAGCGCTGGCAGGTCCGAGAGCTGCGGG  
 TGTGATTAAAGTCCCTGATTTCTC

## **FIGURE 208**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI
PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMMDQLYQGKMYFPGYFPNELRN
IFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP
```

**Signal peptide:**

amino acids 1-15

all other entries from this analysis are longer than 150 amino acids

## **FIGURE 209**

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTTCATGTTCCCTTATTCT  
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGCCTG  
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTGCTGCC  
 ACTGAGGTGGCTGTCATAGGCTTCTCCAGGATTAGAAATACCAAGCAGTGCCATACTCCA  
 TAGCATGGTGCAAAAATTCCCAGGCAGTCATTGGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAAACATCACTGGAACACCCTGCCTCTTCGCCTGGTAGACAATGAACAACTG  
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTCATGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGACTGTGATTGGTTATTCAACAGCG  
 TAATTCAAGATTCACTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
 CACAGATAACCAGAACGGCAGCCAAGCTCTCCAGGGAAAGATTCTCTTATTCTGGTGGACAG  
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG  
 CTTGGCAATTTACCAACTCTAGATGACGAGTGGATACTGCCACAGCAGAACAGTTCC  
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTGGAACTACATATGCC  
 AAGTATCTACTTATGCAAAGTAAAAGGCACAACACTCAAATCTCAGAGACACTAAACAAACAG  
 GATCACTAGGCCTGCCAACACACACACACACAGCTCATTCCCTGTCTAAAATCTCGTTCTC  
 TTCTCCTCTTTAAATTTCATATCCTCACTCCCTATCCAATTCCCTTATCGTGCATT  
 CATACTCTGTAAGCCCACACACACAGAGCTCATTCCCTGTCTAAAATCTCGTTCTC  
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCAATTGTCATTAAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAACATAGTCCCTGCTCTTTAAGGTTACCTAAGGGT  
 TGAAACTCTACCTCTTCTATGACATGTCCGTCTGACTCAGGATAAAAACCAAAGG  
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTGGTTAGCATCTCCAACCTCC  
 TATGTAATCAACAAACCTGCATAATAAAAGGCAATCATGTTATA

## **FIGURE 210**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAAEVAEVEKSSDGPAAQEPWTLDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLIMNKAPEYEENMHRYQKAA
KLFQGKILFILVDGMKENGKVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

**FIGURE 211**

GGAGAGCCGCGGCTGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG  
 GCGGAGAGATCAGAACGCTCTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
 GACCGCGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGGAGCCGG  
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTCTGGCGGGCGCTTGG  
 GCTCTTGACAGCTGGAGTATCAGCCTGGAAGTATACGCCAAAGAAATCTCGTGGCAA  
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
 TCAGTCTCTGGAGCTCCAGCCAGAGGGGGCGACACTACTGTGTCGTTTCCACTACTC  
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG  
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTATACACAATGGCACC  
 TATATCTGTGATGTCAAAAACCCCTCTGACATCGTTGTCAGCCTGGACACATTAGGCTCTA  
 TGTCGTAGAAAAAGAGAATTGCCTGTGTTCCAGTTGGGTAGTGGTGGCAGATTACTG  
 CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTATAGAAGGAAA  
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTGTCACCAGTTAACGAGGC  
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGCTTGTAAAGAGTCTGCCTCTGGATCTCACC  
 AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATT**TAA**GAGAATACTAGAACATATC  
 CTCAGCAAGAAACAAACAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
 AGCCTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA  
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTTTGTACTTTCTTTTC  
 AGGTCAATTACAATTGGGAGATTCAGAAACATTCTTACCATCATTAGAAATGGTTG  
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG  
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
 GCATACCCAGGGTGGCCTTACAGTACAGTACATTATTTGTCTGCCGCTTTAAAAA  
 AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTGAAGTTTCTCACT  
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTAGACTTAAAGTTGCACCCCTG  
 AAATGTGTCAATCAATTCTGGATTCAATAAGCAAGATTAGCAAAGGATAATGCCAAG  
 GTCACTTCATTCTGGACACAGTTGGATCAAACTGATTAAGTAGAAAATCCAAGCTTGCTT  
 GAGAACTTTGTAACGTGGAGAGTAAAAGTATCGGTTTA

## **FIGURE 212**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN
```

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

## FIGURE 213

GCCGGCTGTGCAGAGACGCC **ATG**TACCGGCTCCTGT CAGCAGTGACTGCCCGGGCTGCCGCC  
 CCCGGGGCTTGGCCTCAAGCTGCGGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC  
 TCTCGGCCACGGCTGGGTGGGGCCTCGGGCTGGGGCTGGCGCTGGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGCGCGGCCCCGGCGAGTCCCCCGCGGCCCCGACCCCTGAGGCG  
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCTCGCCCCGTGGTCTCCGAGACCCCGGC  
 GCCGCCCTGCTCCAGGTGCTCGCCAGGCCATCGAGAGCAGCCGACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGCGCACCGGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC  
 TGGTCAGAAGGTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAACCAACAGAGACAGT  
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTTTGCCAAATTGTGGGAAG  
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCGAATTCCAGAAAAAGAA  
 TATGAAGGTGAAAAGGTTCTGTACAACAAGATTACTGATTCCATTAAAGTGGAAATTG  
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
 TGAAAGAGAATGTTGCATTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATT  
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA  
 AAAGAATGATTTGAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT  
 CCCTAAGATTATTTAAAATGATCCTTGTCTTCAAACCTGGTAGTCAGTTTGATTCA  
 ACTTTGGCTATACCCACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAATATTGGA  
 CTATATGCAGAAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
 CAGTGATTTACAATAGAGCAAGG **TAA**ATGAATACCTCTGCTGTCTAGCTATATCGCATC  
 TTAACACTATTTATTAATTAAAAGTCAAATTTCCTTGTCTCATCTGAAAGTGAAGGAAGTAAAACA  
 CACATTGGAGCTTCTACATGTCTGTTCTCATCTGAAAGTGAAGGAAGTAAAACA  
 TGTTTATAAAGTAAAAAAA

**FIGURE 214**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPGLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTAPPSCRCFARAIESRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSITMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR
```

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

## **FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTGGCTCG  
 AGGCTGGTGGGAAGAAGCCGAGA**ATGG**CGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCAGGGCAGCGGCTGCCGGCCGGACT  
 GGTGCGCGAGGGCTGGGGCGGAAGGGTCGAGAGGGCGAGGGCTGTGGCACGGTGGGCTGCT  
 GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACTTCCGAAAGCAGGGCTCACTGCTCT  
 GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGAGCTCAGCGAGGAGGAGCAGGGC  
 CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCAAGGCGACCCGG  
 GCCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTGTCCCTGCGTGCTCCCTGG  
 TGGAGTCGACCTGCGGACCAGCTGACCTGCACGTGGATGTGGCCGGAACGTGGTGGG  
 GTGTCGGTGGTACGCACCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGGA  
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCG  
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG  
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCGTCGTCCCTGTTCTCATGATGTCAGG  
 AGCGCCAGACACCGGGGCCAGGTGGGGTGGGGTGGGGTAGTGGCC  
 TTTGCTGTGCCACCCCTCCCTG**TAA**GTCTATTAAAAACATCGACGATACTGAAATGTG  
 TGAACGTTTGAAAAGCTACAGCTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG  
 TCCTGATGTACAAGCTGATTGAAATTCACTGCTCACTTGATACGTTATTGAGAAACCCAAG  
 GAATGGCTGTCCCCATCCTCATGTGGCTGTGGAGCTCAGCTGTGTTGTGGCAGTTAT  
 TAAACTGTCCCCAGATCGACACGCAAAAAAAA

## **FIGURE 216**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pi: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSARGSGCRAFTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMMSGAPDTGGQ
GGGGGGGGGGSGLCCVPPSL
```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
GGAGCCGGACGTGTCGGGGCGTCCCCGCAGACCGGGCAGCAGGTCGTCCGGGGGCCACC  
**ATG**CTGGTACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGCTGGAACCT  
GTCAAGATGCCGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTCCTCGGTTTC  
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
CTCTATAAAACTTACCAAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTATGTCTG  
TGGCCTTGCCTCTACAGCCTCTTGGCTAGTGGCCTCCTCCCTGTGGATTGGCTGGTC  
GCAAGAATTCTTGTGTCCTCTTCCTCCCTGACTTACTCACTATGCTGCTAACCAAACTCTCT  
CAAGACTACTTGTGCTGCTAGTGGGCGAGCAGTGGTGGCTGTCCACAGCCTGCTCTT  
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCTGCTGAGT  
GGATCCCAGCTACCTTGCTCGAGCTGCCTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCCTGTAGGCCCTTGTGGCTGC  
CATCCCTCTCCTGGCTTGGCAGGGCCTGGCCCTCGAAACTGGGGGAGAACTATGACC  
GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGCGACCGCCGC  
GTGCTGCTGGCACCATAAGCTCTATTGAGAGTGTCTTCATCTTGTCTTCT  
CTGGACACCTGTGCTGGACCCACACGGGCCCCCTGGCATTATCTCTCCAGCTTCATGG  
CAGCCAGCCTGCTGGCTTCCCTGTACCGTATGCCACCTCAAGAGGTACCACTTCAG  
CCCATGCACCTGCTGTCCTTGCTGTGCTCATCGTCGTCTCTCTCTTCATGTTGACTTT  
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT  
TGGCTTGTGGATTATACTTCCCAGCATGAGCTTACGGAGAAAGGTGATCCCTGAGACA  
GAGCAGGCTGGTGTACTCAACTGGTCCGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
CCTTGTCCCTCATGACAGTGTGATCGAAAAACAGGCACTCGGAATATGTTCAGCATTGCTCTG  
CTGTCATGGTGTGATGGCTCTGCTGGCAGTGGTGGACTCTCACCGTGGTAAGGCATGATGCT  
GAGCTGCGGGTACCTCACCTACTGAGGAGCCATGCCCTGAGCTG**TAA**CCCCACTCCAG  
GACAAGATAGCTGGACAGACTCTGAAATTCCAGCTATCGGGATTGTACAGATCTCTGT  
GACTGACTTTGTGACTGTCCTGTGGTTCTCCTGCCATTGCTTGTGTTGGGAGGACATGA  
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTCCCTCTGTGTTACTCCCATTAGAAA  
ATAAACACTTTAAATGATCAAAAAAAAAAA

## **FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARA\_AFWNHVIAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCILLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET  
EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAVVGLFTVVRHDA  
ELRVPSPTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

## **FIGURE 219**

GCGACCGCGCGGGGGCGCGAGAGGAAACCGCGCCGGGCCGGCCCTGGAGATG  
GTCGGCGCCGGCTGGTGTCTCGTCTGGCTCCCCGCGTGCCTCGCGGCCA  
CGGCTTCCGTATCCATGATTATTGTACTTCAAGTGCTGAGTCCTGGGACATTGATACA  
TCTTCACAGCCACACCTGCCAAGGACTTGGTGGTATCTTCACACAAGGTATGAGCAGATT  
CACCTTGTCCCCGCTGAACCTCCAGAGGCCCTGCCGGAACTCAGCAACGGTTCTCATCCA  
GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC  
AGGAGCACGGCGGGCGGGCGGTGATCATCTGACAACGCAGTTGACAATGACAGCTTCTAC  
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCCCTGCTCGG  
CCGAGACGGCTACATGATCCGCCCTCTGGAACAGCATGGCTGCCATGGGCCATCATT  
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCTGCAACCGCCCTGGACCTTC  
TGGTAGAAGAGTTGCTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGAAACCC  
AGGAATTGCTACTTGAATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA  
AAAGGGTTGGCGTTGCTAGGCTGAAAGGGAGCCACACCCTGGCCTCCCTCCCCAGG  
GCCCAAGGGTGTCTCATGCTACAAGAAGAGGAAGAGACAGGCCAGGGCTCTGGCTA  
GAACCCGAAACAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
CACCTGGCTCCAGCCTCCCTACCCAGGGTCTCTGCACAGTGACCTCACAGCAGTTGTTGG  
AGTGGTTAAAGAGCTGGTGTGGGACTCAATAAACCTCACTGACTTTAGCAATAAA  
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIIISIPVNVTISIPTFELLQPPWTW
```

### Signal peptide:

amino acids 1-20



## **FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGC
HCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVF
NVIYLENEDSE
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

## **FIGURE 223**

CTCGCTTCTCCTTCTGGATGGGGGCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGC~~CCGG~~CACAACCAGACGCCAGTCACAGGCAGAGCCCTGGG**ATG**CACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGC~~CC~~CCTGGGGGCCACCTGGCAGGGAAAGATGTAT  
GCCCTGGAGGAGGCAAGTATTTCAGCACCAGTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCCTGGTAAAAGTGTCCAGGTGAAACTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTAGGTGGGAAATACCCAGGAAGTCACCC~~T~~GCAGCCAGGCGAATAC  
ATCACAAAAGTCTTGT~~CG~~CTTCCAAGCTTC~~CC~~GGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTCTATTGGAGCTTGATGCCAGATCTCCTGC~~CT~~ACCCCAGCCAAG  
AGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACC~~ACT~~GAGCCACCAGTTAATCTCACATACTC  
AGCAA~~ACT~~ACCCGTGGTC~~CG~~**TAG**GGTGGGTATGGGCCATCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTA~~CT~~GAGTCGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTCTGCAGAAAA

### **FIGURE 224**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPAGGKYFSTTEDYDHEITGLRVSGLLLVKSVQVK
LGDSDVKGALGGNTQEVTLQPGEYITKVFVAFQAFRLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

### Signal peptide:

amino acids 1-22

## **FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCCTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAACTGGGTGCTCATCACGGAACTGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCCTGGAAGAATACATCATGTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
 TTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAACTGTAAGATGCAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTGATGTTGCTGCGAATGCGGTGTTGGATT  
 TATTGTTCTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTCAAAATCGGTCCATCT  
 CCCAAGGGGTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGGCTGTCATGCAACTGGCCCCTAACGCAAAGACCTAACGGACGACCTTGAA  
 CAATACAAAGGATGGGTTCAATGTAATTAGGTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCACTGCTTACTGACAATGCTTCTTGCGAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTAAGTA  
 TATCTGCTGGTTGCTTAGGTTGTCCTCGCTATAACAGCCTCAAAAACCTTAAGTATAAT  
 CAATTTAAAGGGCTAACCGAGCTCACCTGGCTACCTGACCATAACCATAACGCAATAT  
 TGACGAAAATGCTTTAATGGAATACCGAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
 TCTCCTATTTCTAACATAACCTCAGACCTGTGACAAATTACGGAACTTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGATCTGAACAGTTGCGGCTTGCGGAAGCTGCTGAGTT  
 ACATTTACGGTCTAACCTCCCTGAGAACCATCCCTGTGCGAACATTCCAAGACTGCCGCAACC  
 TGGAACTTTGGACCTGGATATAACCGATCCGAAGTTAGCCAGGAATGTCTTGCTGGC  
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTCAGCTAACCTGGCCCT  
 TTTCCAAGGTTGGTCAGCCTCAGAACCTTACTTGCACTGGATAAAATCAGTGTCAAG  
 GACAGACCATGTCCTGGACCTGGAGCTCCTAACAAAGGCTTGATTATCAGGCAATGAGATC  
 GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCTGAATCTGCAGCGCCTAACCTGG  
 TTCCAACAAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA  
 TCAGTCTGCTGGAAATATGGGAATGCAGCAGAAATATTGCTCCCTGAAACTGGCTG  
 AAAAGTTAAAGGTCTAAGGGAGAAATACAATTATCTGTGCCAGTCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT  
 TTGATCTGCCAGGGCTCTCCAAAGCCGACGTTAACGCCAACGCTCCCCAGGCCGAAGCAT  
 GAGAGCAAACCCCTTGCCCCCGACGGTGGAGCCACAGAGCCGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTCTGTCCG  
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCACTGGAAAGCGGTACCCCTGCGAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAACAGGACAGGAAAAAGACAGTCCTAAAGCAAAT  
 GACTCCCAGCACCCAGGAATTATGAGATTATAACCCACCAACACGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
TGAACCATTGTGATAAAAAGAGCTCTAAAGCTGGGAAATAAGTGGTGTCTTATTGAACTC  
 TGTTGACTATCAAGGGAACCGCATGCCCTCCCTCCCTCCCTCACTTGGTGG  
 CAAGATCCTCCTGTCGTTAGTGCATTATAACTGGTCATTCTCATACATA  
 ATCAACCCATTGAAATTAAATACCACAATCAATGTGAAGCTGAACTCCGGTTAATATAA  
 TACCTATTGTATAAGACCCTTACTGATTCCATTAATGTCGCATTGTTAAGATAAAACT  
 TCTTCATAGGTAAAAAA

**FIGURE 226**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pi: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMWYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLAFLPRLVSLQONLYLQWNKISVIGQTM
SWTWSSLQRDLDSGNEIEAFSGPSVFQCPNLQRLNLDNSNKLTFIGQEILDWSISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPKPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPSTQEYVVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV

```

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCTAAGTTGACTGTCCTT  
 TAAATATGTCAGATCCAGACTTTCACTGTCACCTCAGCGATCTAACGATAGGGATCTG  
 TGGTGCCTGCTATTCCAGTTGGTGCCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
 AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTGG  
 TGGCAGCTCTCTGTGGAGCTGTGGTCCCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
 ATTGATTCTCACAGGCGCACCATGGCAGTTTGCTGTTGGAGACTGGACTCTATTATGG  
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTCAAACCTCAAACCCCTGACCTAT  
 ATCCTGTTCTGCTCCATGTTGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
 AAAACAACCTGAATTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA  
 AAACATCAAATTAGGAATAGTTATTCACTGTTGGAAATGTCCAGAGATCTATTCACTATA  
 GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTTGGAAAAAAATTGGTCACTGGAGATG  
 TTTAAATAGTAAAGTAGCAGGCTTTGATGTGTCAGTGCTGTATCATACTTTATGCTACAC  
 AACCAAATTAAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
 TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTCTTC  
 CTAGCATGGGTCCATAAAATTATAATTAAACATAGGCCAAGCCGAGAATCCAACAT  
 GTCCAGAACCAAGAACAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
 CAGCAAAACAAGAGGTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGAGAAAAGAAAATTCCC  
 CTTTACAGTAATGAATGTGGCCTCCATAGTCATAGTGTGTTCTGGAGCCTCAGGGCTG  
 GCATTTATTGCAAGCATCATGCTAAGAACCTCGGCATAGGTATCTGTTCCATGAGGACTGC  
 AGAAGTAGCAATGAGACATCTCAAGTGGCATTGGCAGTGGCCATCAGCAGGGGACAGA  
 CAAAAACATCCATCACAGATGACATATGATCTCAGTGACAAATTGTTGAACAAAACAAT  
 AACATCAATAGATATCTAAAAA

## **FIGURE 228**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVILCLQCWLRRPRIDSHRRTMAVFAVGDLDIYGTEAAVSPPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

**FIGURE 229**

GAGCGGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCACTCCCACCCACCGGCCT  
 TTCTCCAGCTCGATCTGGAGGCTGCTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA  
 GCTCTCGCTCGCTGCCCGCTCAGAACGCTCCGTGGCGGGCAGCGTACGAGAACGCC  
 ACGGCCAGCTCAGTCTCTTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTAAACT  
 CCCTCTCAAAACTCATCTCCTGGGTACTGAGTTAATAGAGTGGATAACACCTGCTGAAG  
 ATGAAGAATATAACATATTGAGGATTTTTCTTTCAAGTCTTGATTGTGGC  
 TTACCTCAAGTTACCATTTTCAGTCAGTCAGTCTGTTGTTGCTCTTCAGAA**ATG**TTTTA  
 CAATCTCAAGAAAAAAATATGCCCAGAAATTGAGTTACTGTTGCTGTATTGGACTCATT  
 TGGGATTGATGTTACTGCACTATACTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTCTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT  
 GCTGTCCTCTGGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
 TGGTGTGAATGGCTCAGCAGCCAACACCAATGGTACTAGTGGAAATTGGTGCCAGTAA  
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGA**TAG**CAGTTGAAATCACCTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTCAAGGAGTATGCTGGATTATGGAAC  
 TCTAATTCTGTACATAAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG  
 CTGTAATGTCCTAAAGAGAATTGGTAACCTGGTGTGAGCAGATAGGTGAGT  
 TTTGTATAATCTTTGTGTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTCA  
 ATTCTATAACACATTATAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAA  
 TCATTCTGTCAATTGTTCTCAATAGATGTAATGTTAGACTACGGCTATTGAAAAATGTG  
 CTATTGTAATATTGTTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTGAATCATGACCCAAAGAACATGATTGATTGCACTATCCTTCAGAATAACTGA  
 AGGTTAATTATTGTATATTAAAAATTACACTTATAAGAGTATAATCTGAAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGCAATTAAATAACAGCATTAAAGTT  
 GTAAACTCTAATCTTAACTTATTGAAGAATAAAAGATATTGTTATGAGAGTAACAATA  
 AAGTATTGATTGATTGTTACATACATGAATGTTATTAAAGTTAATCCTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTGTTCCATATTGGGTTAATTGCTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTGGAGAATGGAACCTTGAGGACTTGTGAGGAGTATATAAAA  
 GGTACTTTGTGCTGCATTAATTGCTGGAAAGTGTAAACATTATATTATAAGAGTATC  
 CTTATGAAATTGTAATTGTATAACAGATGCATTAGATATTCAATTATATAATGGCAC  
 TTAAGAATGAAACATTAAATATAAAACTATGAAGAGATTGACTATCTTTCAGGAAAAAGCT  
 GTATATAGCACAGGAAACCTAATCTGGGTAAATTCTAGTATAAAACAAATTATACTTTAT  
 TTAATTTCCCTGTAGCAAATCTAATTGCCACATGGTGCCTATATTCAAGTATTATT  
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTAGATTAGACTATATAGAATTAGATAT  
 TGTATTGTCGTCAATTATAATGCTACACATGTAGCAATAATTACAATATTATTAAAA  
 TAAATATGTGAAATATTGTTCATGAAAGACAGATTCCAATCTCTTCTCTGTAC  
 CTGTCTACCTTATGTGAAGAAATTAAATTATGCCATTGCCAGGT

## **FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSSLLVFGGLIWLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTNGTSGNL
VPVTTNKRTNVSGSIR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

## **FIGURE 231**

CGCGGCCGGGCCGGGGTGAGCGTGCCGAGGC GGCTGGCGCAGGCTTCCAGCCCCCAC  
CATGCCGTGGCCCCCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCATGCT  
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTCGACAGCTTCAGCCTGACTCGG  
 GTGGATTGTAGCGGCCCTGGGCCCCACATCATGCCGGTGCCCATCCCTGGACACAGCCA  
 CTTGGACCTGTCCCTCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGCCGGGCT  
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACTGCTCACCAGCATCTCACCCACTGCC  
 TTCTCCC GCCCTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCTGCC  
 AGCCGAGAGCTCACCAAGCTCACCCCTGAGCGACGTGAACCTAGCCACAACCAGCTCCGGG  
 AGGTCTCAGTGTCTGCCTTCACGACGACAGTCAGGGCCGGGACTACACGTGGACCTCTCC  
 CACAACCTCATTCAACCGCCTCGTCCCCACCCACAGAGGGCCGGCTGCCCGCACCACAT  
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
 TCGCCTACCTGAGCCTGGATGGAACCCCTAGCTGTATTGGTCCGGTGCCTCGCGGGG  
 CTGGGAGGCCTTACACACCTGCTCTGGCCAGCCTGAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTGGACCTGTCGGCAACCCAAGCTTAAC  
 GGGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGAGGAGCTGGACCTTCGGGCACC  
 AACCTGGTGCCCTGCCTGAGGCGCTGCTCCACCTCCGGCACTGCAGAGCGTCAGCGT  
 GGGCCAGGATGTGGGTGCCGGCGCCCTGGTGCGGGAGGGCACCTACCCCCGGAGGCCTGGCT  
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGAATCTGCTGCCAGGGCCCCACC  
 ATCTTG**TGA**CAAATGGTGTGGCCAGGGCACATAACAGACTGCTGTCCTGGCTGCCCTCAG  
 GTCCCGAGTAACCTATGTTCAATGTGCCAACACCAGTGGGGAGCCGCAGGCCTATGTGGCA  
 GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTGGACCTGGAGCCACACCTAGGAGC  
 AAAGTCTCACCCCTTGTCTACGTTGCTTCCCAAACCATGAGCAGAGGGACTCGATGCCA  
 AACCAGACTCGGGTCCCCTCCTGCTCCCTCCCCACTTATCCCCAAGTGCCTCCCTCAT  
 GCCTGGGCCGGCTGACCCGCAATGGCAGAGGGTGGTGCGGCCCTGCTGCAGGGCAGA  
 GTTCAGGTCACACTGGCCTGAGTGTCCCCCTGGGCCATGGCCAGTCAGGGCGAGTT  
 TCTTTCTAACATAGCCCTTCTTGCCATGAGGCCATGAGGCCGCTTCATCCTTTCTAT  
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTCTATGTGAC  
 AGATGGGAAACTGAGGCCTTGAGAAGGAAAAGGCTAATCTAAGTCCCTGCGGGAGTGGC  
 ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCGGACCAATGCACCTTCTGTCTCCTCTA  
 ATAAGCCCCACCCCTCCCCGCTGGCTCCCTGCTGCCCTGCCATTAGCACA  
 GGAGTAGCAGCAGCAGGACAGGAAGAGCCTCACAAAGTGGGACTCTGGCCTCTGACCAGCT  
 GTGCGGCATGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAAGCTTAGGGCACATTGGTT  
 CCAGCCTAGCCAGTTCTCACCCCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACC  
 CATTTCCTCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTCTGGAGCCTCA  
 TCTGGCTGGATCTCAAGGGCCTCTGGATTCAAGTCCCCTGGCCCTGAGCACAGCAGC  
 CCTTCTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC  
 TCTACCCCAAGGGCAGCCTCAGCTCCGAACCCCTGGCTGTTCTTAGTCTCATTTA  
 TAAAAGTTGTCCTTTAACGGAGTGTCACTTCAACCGGCCTCCCTACCCCTGCTGGC  
 CGGGGATGGAGACATGTCATTGTAAGCAGAAAAAGGTTGCATTGTTCACTTTGTAAT  
 ATTGTCCTGGGCTGTGTTGGGTGTGGGGAGCTGGCAGTCAGTGGCCACATGGGCATC  
 AGGGGCTGGCCCCACAGAGACCCCCACAGGGCAGTGAAGCTCTGTCTCCCCCACCTGCC  
 CCATCATCTAACC GGTCCTGATTAAATAACACTATAAAAGTTAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pi: 6.80, NX(S/T): 2
MPWPLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDSLHNLIHRLVPHPTRAGLPPTI
QSLNLAWNRLHAVPNLRDPLRLYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGLQVLDLSGNPKLNWAGAEVFSGLSSIQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

## FIGURE 233

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCTCCCCAGTTCCCTGTGGGTCTGAGG  
 GGACCAAGGGTGAGCTACGGCTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
 AAACAAGTTGACATTCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCTGCT  
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGGCCAGGATGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTTCAC  
 GGGAGGCTTGGCAGTTTCTTACTCCTGTGGCTCCAGATTCAAGGCTAAGATGAAAGCC  
 TCTAGTCTGCCTCAGCCTCTCTGCTGCGTTATCTCTATGGACTCCTCACTGG  
 ACTGAAGACACTCAATTGGGAAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATG  
 GATTTCTGAGATACTGGGAGTGTGCAAGCAGGAAAGATGGAAACATTGACATCAGAATCTTA  
 AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCTGCCATT  
 GCTAAGACTCTATCTGGACAGGGTATTAAAAACTACCAGACCCCTGACCATTATACTCTCC  
 GGAAGATCAGCAGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCAT  
 GCCCACATGACATGCCATTGTGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGTTGGGAACTAGACATTCTTC  
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGTGCTGCTAAGAATATTGAGGT  
 CAAGAGCTCCAGTCTCAATACCTGAGAGGAGGATGACCCAAACCACCATCTCTTACT  
 GTACTAGTCTGTGCTGGTACAGTGTATCTTATTCATGCATTACTTGCTCCTGCATGAT  
 TGTCTTATGCATCCCCATCTTAATTGAGACCATACTGTATAAGATTTGTAATATCTT  
 TCTGCTATTGGATATTTATTAGTTAATATATTATTATTGCTATTAAATGTATTT  
 ATTTTTTACTGGACATGAAACTTAAAAAAATTCAAGATTATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTATACAGTAAAAAAAAACCTGTAATTCTAGAAGAGTGGCT  
 AGGGGGTTATTCAATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA  
 TATTGAAATTGAACCAATGACTACTAGGATGGGTTGGAATAAGTTGATGGAATT  
 GCACATCTACCTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCATAATTGTGTAT  
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTCTTCATA  
 CCAAAAAAAAAAAAAAAA

## **FIGURE 234**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pi: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSILLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCCTACTGCTGAATGTCCGTCCGGAGGAGGAGAGGCTTTGCCG  
CTGACCCAGAGATGCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGGGCTACCGTGGC  
CGAGCTAGCAACCTTCCCGATCTCACAAAAACTCGACTCCAAATGCAAGGAGAACAG  
CTCTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCTATAGGGGAATGGTGCGCACA  
GCCCTAGGGATCATGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCGAGAGGTTG  
TGTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTATTGCCAGTTAGCCAATCCAAC TGACCTAGTGAAGGTTCAGATGCAAAT  
GGAAGGAAAAGGAAACTGGAAGGAAAACCATTGCGATTCTGGTGTACATCATGCATTG  
CAAAATCTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCAATATAACAA  
AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGATACTGAAACACTACTGGT  
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC  
TGGTAGCTCTATTCTGGAACACCAGCCATGTCATCAAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAAAGGAAGGGACTTTGTATAAATCATGACTGACTGCTTGATTAGGCTGT  
TCAAGGTGAAGGATTCACTGAGTCTATATAAGGCTTTACCATCTGGCTGAGAATGACCC  
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
TTTTAA

## **FIGURE 236**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEH
YPLWKSIVGGMMAGVIGQFLANPTDLVKVQMQUEGKRKLEGKPLRFRGVHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLNTPLEDNIMTHGLSSLCGLVASILGTP
ADVIKSrimnQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## FIGURE 237

CGGACGCGTGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTCCTGCGCGC  
 GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGATAACAGCATTAAATGAAAAATTATGC  
 TTAAGAAGTAAAA**ATG**GCAGGCTCCTAGATAATTCGTTGCCAGAATGTGAATGTATTG  
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGCGCAGGTATATTGTTTTACAGGC  
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAACGCCAGAACAGTTGAACCATGCCT  
 TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC  
 AGGTGAGAGGTGATAAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCT  
 TTCATTGGTTCATGTTGATGTTGGGTCACTTATTGCTCCATGTGGATTCTTTGGTGC  
 ATATGTTACCCAAAATACTGATGTTATCCGGGACTAGCTGTGTTTCAAAATGCACTTA  
 TATTTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACC**TGA**GATCAC  
 TTCTTAAGTCACATTTCTTTGTTATATTCTGTTGAGATAAGGTTTATCTCTCAGT  
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTGTTCATTACATTATGTT  
 TGAGTTTGAAATAGTTATGAAATTCTTATTTTCATTGCATAGACTGTTAATATGTA  
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTATTCCCTGAGATTAGAA  
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTGTCATTAGAAGTAACCACTCTTGT  
 CTCTCTGGCTGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTGGGAGGCCGAGGCC  
 CCGATTGCTTGAGGTCAAGTGGTGGACAGCCTGGCCAACATGGCGAAACCCCATCTACT  
 AAAAATACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
 TGAGGCAGGAGAATCGCTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCGCCAC  
 TGCACCTAGCCTGGGGAGAAAGTGAAAACTCCCTCTCAAAAAAAAGACCACTCTCAGTATC  
 TCTGATTTCTGAAGATGTACAAAAAAATAGCTCATATATCTGGAATGAGCACTGAGCCA  
 TAAAAGGTTTCAGCAAGTGTAACTTATTGGCCTAAAATGAGGTTTTGGTAAAGA  
 AAAAATATTGTTCTATGTATTGAAGAAAGTGTACTTTATATAATGATTAAATGCC  
 AAAGGACTAGTTGAAAGCTTCTTAAAAAGAATTCTCTAATATGACTTATGTGAGAA

## **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVAVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

## FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGCCCGAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCAGGGTGGT  
 GGTCAAGCTGGGTCAAGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAACAG  
 GGAAGTGGGAGCCTCGAGCCCTGGGTGGAAGCTGACCCAAGCCACCCCTCACCTGGACAG  
**GATG**AGAGTGTCAAGGTGTGCTCGCCTCTGGCCCTCATCTTGCCATAGTCACGACATGGA  
 TGTTTATTCAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCCACCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC  
 AGCCAACACTTTGCCTTAAAATCTGCAGTGGGCCGCAACGTGTTGGCCCTACTATGT  
 GCTTGAAAGACCGCATGATCATGAGTCTGTGAAAAAACATGTGGCAGAGGCCTAACATC  
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGTGGTGG  
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTGACTTG  
 GGGAGTTCCACGCAAAACAACGGGCTTGGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACG  
 CCTCAGGGGTAAAAGCCCCTTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACG  
 AGGGATGGCCAGAGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATT**TAGGGTGGC**  
 TGTGGCTCTCCTCAGCCAGGGCCTGAAGAACGCTCTGCCTGACTTAGGAGTCAGAGCCCG  
 GCAGGGGCTGAGGAGGAGCAGGGGTGCTGCGTGGAAAGGTGCTGCAGGTCTGCACGC  
 TGTGTCGCCCTCTCCTCGAAACAGAACCCCTCCACAGCACATCCTACCCGGAAAGACC  
 AGCCTCAGAGGGCTTCTGGAACCAGCTGTGAGAGAATGGGTGCTTCGTCAGGG  
 ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCAAATTAAATTAA  
 TTTTGCTGGTTTGAAAAA

## **FIGURE 240**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

## **FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCCTGGGAT  
 CCAGAAACCCATGATACCTACTGAACACCGAATCCCTGGAAGCCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCAGTCCC  
 CTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTGCTGGAGGTGATTGGATCC  
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGCCA  
 GCCTCTTACCCCTGAGTGTGAAACAATGCCAGCTGCCATCGATATTCAAGACAGACAGTGT  
 GACATTGACCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
 CTTGGACCTGCACAACAATGCCACACAGTGCAACTCTCTGCCCTTACCCCTGTATCTG  
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGTGAGAAAGGATC  
 CCCAGGGGGTCAGAACACCCAGATCAACAGTGAAGCCACATTGAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCTGGCT  
 GTCCTGGGCATCCTAATTGAGGTGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
 TCACCTGCATGAAGTCAGGCATAAAGATCAGAACGACTCAGTGCTCCCTAACCTAACAGAG  
 AGCTGCTCCCCAACAGCTGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT  
 TGCTACCAGAGTGTGCTGGACAGTTTTATAGAAGGTCCCAGATTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAACAGGAGGCCCTCTAACGCTTCTGGTACAGA  
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGCTTGCTCTTCATCCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTGGTGGCTGTCTG  
 CCTTCTCCTGGCTGTTATTCATTGCTAGAAAGATTCGGAAGAACAGGCTGGAAAACCGAA  
 AGAGTGTGGTCTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCCTCTCAGATAACCA  
 TGGATGTGGATGACTTCCCTCATGCCTATCAGGAAGCCTCTAAAATGGGGTAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTTAGAGAG  
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACACTGCAGAGCCTCAGCCTCTCAAACATGTA  
 GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTCTGTTAGTTGCAGGG  
 GAAGTTGGATATAACCCAAAGTCCTCTACCCCTCACTTTATGGCCCTTCCCTAGATA  
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTGATCAATA  
 TATTGGAAATTAAAGTTCTGACTTT

## FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## FIGURE 243

AATTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCCTC  
GTGGACCCAAAGGTAGCAATCTGAAAC**ATG**AGGAGTACGATTCTACTGTTGTCTCTAGG  
ATCAACTCGGT CATT ACCACAGCTCAAACCTGCTTGGGACTCCCTCCCACAAA ACTGGCTC  
CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTCCTTAAAGTCTG  
ATACCATTAAACACAGATGCTCACACTGGGCCAGATCTGCATCTGTAAATCCTGCTGCAGG  
AATGACACCTGGTACCCAGACCCACCCATTGACCCCTGGGAGGGTTGAATGTACAACAGCAAC  
TGCACCCACATGTGTTACCAATTTCGTACACAACTTGGAGGCCAGGGCACTATCCTAAGC  
TCAGAGGAATTGCCACAAATCTCAGCAGCCTCATCATCCATTCTGTTCCCGGGAGGCAT  
CCTGCCACCAGTCAGGCAGGGCTAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAG  
GAGCAGGTGTAATCCTGCCACCCAGGGAACCCCAGCAGGCCGCTCCAACTCCCAGTGGC  
ACAGATGACGACTTGCA GTGACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA  
GGAAGCCACCACAGAACAGCAAATGGAATTCA**TAA**GCTGTTCAAATTTCAACTAAG  
CTGCCTCGAATTGGTGATACATGTGAATCTTATCATTGATTATATTGGAATAGATTGA  
GACACATTGGATAGTCTAGAAGAAATTAAATTCTTAATTACCTGAAAATATTCTTGAAATT  
TCAGAAAATATGTTCTATGTAGAGAACCTTAAACAACTTAAACATAATTCAATGGATAAAAT  
CTGTCTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAAACATATTGGAAA  
ACTGGAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA  
AAAAAAAAA AAAAAA

## **FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGT PAGRLPTPSG  
TDDDFAVTPAGIQRSTHAIIEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCAGCGGCCTCGGAGCGCGCG  
 GAGCCAGACGCTGACCACGTCCTCTCCTCGGTCTCCGCCTCCAGCTCCGCCTGCCCG  
 GCAGCCGGGAGCC**ATG**CGACCCCCAGGGCCCCGCCCTCCCCGCAGCGGCTCCGCAGGCCTCC  
 TGCTGCTCCTGCTGCTGCAGCTGCCCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG  
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGCCAATGTTATTCCGGTACACCTG  
 GGATCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAG  
 GAGTCCTGGACACCCAACATACAAGCAGTGTTCATGGAGTTCAATTGAATTATGGCATAGATCT  
 TGGAAAATTGCGGAGTGTACATTACAAAGATGCGTTCAAATAGTGCCTAAGAGTTTGAG  
 TCAGTGGCTCACTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTCACATT  
 AATGGAGCTGAATGTTAGGACCTCTTCCCATTGAAGCTATAATTATGGACCAAGGAAG  
 CCCTGAAATGAATTCAACAATTAAATTACATCGCACTCTCTGTGGAAGGACTTGTGAAG  
 GAATTGGTGGATTAGTGGATGTTGCTATCTGGTTGGCACTGTTCAAGATTACCAAAA  
 GGAGATGCTCTACTGGATGGAATTCAAGTTCTGCATCATTATTGAAGAACTACCAAAA**TA**  
**A**ATGCTTAATTTCATTGCTACCTCTTTTATTATGCCTGGAAATGGTCACTTAAAT  
 GACATTTAAATAAGTTATGTATACTGAAATGAAAAGCAAAGCTAAATATGTTACAGA  
 CCAAAGTGTGATTCACACTGTTTAAATCTAGCATTATTCAATTGCTCAATCAAAGT  
 GGTTCAATATTTTTAGTTGGTTAGAATACTTCTCATAGTCACATTCTCAACCTA  
 TAATTGGAATTGTTGTGGCTTTGTTCTTAGTATAGCATTAAATTTAAAAATA  
 TAAAAGCTACCAATCTTGTACAATTGTAAGAATTTTTATATCTGTTAAAT  
 AAAAATTATTCCAACA

## **FIGURE 246**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSYPKGDASTGWNSVSRIIIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217